

SEQUENCE LISTING

<110> Ruben, Steven M.
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Gruber, Joachim R.
Dillon, Patrick J.
Gentz, Reiner L.

<120> Keratinocyte Growth Factor-2

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<170> PatentIn Ver. 2.1

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Pro Gly Cys Cys Cys Cys Cys Phe Leu Leu Leu Phe Leu Val Ser Ser
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gtc cct gtc acc tgc caa gcc ctt ggt cag gac atg gtg tca cca gag 144
Val Pro Val Thr Cys Gln Ala Leu Gly Gln Asp Met Val Ser Pro Glu
35 40 45

gcc acc aac tct tct tcc tcc tcc ttc tcc tct cct tcc agc gcg gga 192
Ala Thr Asn Ser Ser Ser Ser Ser Phe Ser Ser Pro Ser Ser Ala Gly
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agg cat gtg cgg agc tac aat cac ctt caa gga gat gtc cgc tgg aga 240
Arg His Val Arg Ser Tyr Asn His Leu Gln Gly Asp Val Arg Trp Arg
65 70 75 80

aag cta ttc tct ttc acc aag tac ttt ctc aag att gag aag aac ggg 288
Lys Leu Phe Ser Phe Thr Lys Tyr Phe Leu Lys Ile Glu Lys Asn Gly
85 90 95

aag gtc agc ggg acc aag aag gag aac tgc ccg tac agc atc ctg gag 336
Lys Val Ser Gly Thr Lys Lys Glu Asn Cys Pro Tyr Ser Ile Leu Glu
100 105 110

ata aca tca gta gaa atc gga gtt gtt gcc gtc aaa gcc att aac agc 384
Ile Thr Ser Val Glu Ile Gly Val Val Ala Val Lys Ala Ile Asn Ser

115	120	125	
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130	135	140	
gaa ttt aac aat gac tgt aag ctg aag gag agg ata gag gaa aat gga			480
Glu Phe Asn Asn Asp Cys Lys Leu Lys Glu Arg Ile Glu Glu Asn Gly			
145	150	155	160
tac aat acc tat gca tca ttt aac tgg cag cat aat ggg agg caa atg			528
Tyr Asn Thr Tyr Ala Ser Phe Asn Trp Gln His Asn Gly Arg Gln Met			
165	170	175	
tat gtg gca ttg aat gga aaa gga gct cca agg aga gga cag aaa aca			576
Tyr Val Ala Leu Asn Gly Lys Gly Ala Pro Arg Arg Gly Gln Lys Thr			
180	185	190	
cga agg aaa aac acc tct gct cac ttt ctt cca atg gtg gta cac tca			624
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 35 40 45
 Ala Thr Asn Ser Ser Ser Ser Phe Ser Ser Pro Ser Ser Ala Gly
 50 55 60
 Arg His Val Arg Ser Tyr Asn His Leu Gln Gly Asp Val Arg Trp Arg
 65 70 75 80
 Lys Leu Phe Ser Phe Thr Lys Tyr Phe Leu Lys Ile Glu Lys Asn Gly
 85 90 95
 Lys Val Ser Gly Thr Lys Lys Glu Asn Cys Pro Tyr Ser Ile Leu Glu
 100 105 110
 Ile Thr Ser Val Glu Ile Gly Val Val Ala Val Lys Ala Ile Asn Ser
 115 120 125
 Asn Tyr Tyr Leu Ala Met Asn Lys Lys Gly Lys Leu Tyr Gly Ser Lys
 130 135 140
 Glu Phe Asn Asn Asp Cys Lys Leu Lys Glu Arg Ile Glu Glu Asn Gly
 145 150 155 160
 Tyr Asn Thr Tyr Ala Ser Phe Asn Trp Gln His Asn Gly Arg Gln Met

	165		170		175										
Tyr	Val	Ala	Leu	Asn	Gly	Lys	Gly	Ala	Pro	Arg	Arg	Gly	Gln	Lys	Thr
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35 40 45
Ser Leu Val Ala Leu Ser Leu Ala Arg Leu Pro Val Ala Ala Gln Pro
50 55 60
Lys Glu Ala Ala Val Gln Ser Gly Ala Gly Asp Tyr Leu Leu Gly Ile
65 70 75 80
Lys Arg Leu Arg Arg Leu Tyr Cys Asn Val Gly Ile Gly Phe His Leu
85 90 95
Gln Ala Leu Pro Asp Gly Arg Ile Gly Gly Ala His Ala Asp Thr Arg
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Asp Ser Leu Leu Glu Leu Ser Pro Val Glu Arg Gly Val Val Ser Ile
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Phe Gly Val Ala Ser Arg Phe Phe Val Ala Met Ser Ser Lys Gly Lys
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 Glu Ser Gly Tyr Leu Val Gly Ile Lys Arg Gln Arg Arg Leu Tyr Cys
 65 70 75 80
 Asn Val Gly Ile Gly Phe His Leu Gln Val Leu Pro Asp Gly Arg Ile
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 100 105 110
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 Tyr Glu Ser Asp Leu Tyr Gln Gly Thr Tyr Ile Ala Leu Ser Lys Tyr
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 35 40 45
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Gln His Ile Ser Thr His Phe Leu Pro Arg Phe Lys Gln Ser Glu Gln 210 215 220		
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35 40 45
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50 55 60
Gln Ala Glu Glu Arg Gly Val Val Ser Ile Lys Gly Val Cys Ala Asn
65 70 75 80
Arg Tyr Leu Ala Met Lys Glu Asp Gly Arg Leu Leu Ala Ser Lys Cys
85 90 95
Val Thr Asp Glu Cys Phe Phe Phe Glu Arg Leu Glu Ser Asn Asn Tyr
100 105 110
Asn Thr Tyr Arg Ser Arg Lys Tyr Thr Ser Trp Tyr Val Ala Leu Lys
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Thr	Ile	Gln	Gly	Thr	Arg	Lys	Asp	His	Ser	Arg	Phe	Gly	Ile	Leu	Glu
				85					90					95	
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Ala	Lys	Lys	Glu	Cys	Asn	Glu	Asp	Cys	Asn	Phe	Lys	Glu	Leu	Ile	Leu
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Glu 145	Phe	Asn	Asn	Asp	Cys 150	Lys	Leu	Lys	Glu	Arg 155	Ile	Glu	Glu	Asn	Gly 160	
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50 55 60
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Val Glu Val Gly Ile Val Ala Ile Arg Gly Leu Phe Ser Gly Arg Tyr
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Leu Ala Met Asn Lys Arg Gly Arg Leu Tyr Ala Ser Glu His Tyr Ser
100 105 110
Ala Glu Cys Glu Phe Val Glu Arg Ile His Glu Leu Gly Tyr Asn Thr
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Leu Phe Leu Pro Arg Val Leu Asp His Arg Asp His Glu Met Val Arg
180 185 190
Gln Leu Gln Ser Gly Leu Pro Arg Pro Pro Gly Lys Gly Val Gln Pro
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 Lys Gly Arg Pro Arg Lys Gly Ser Lys Thr Arg Gln His Gln Arg Glu
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 Val His Phe Met Lys Arg Leu Pro Arg Gly His His Thr Thr Glu Gln
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                    70                      75                      80

ttc tct ttc acc aag tac ttt ctc aag att gag aag aac ggg aag gtc 886
Phe Ser Phe Thr Lys Tyr Phe Leu Lys Ile Glu Lys Asn Gly Lys Val
                    85                      90                      95

agc ggg acc aag aag gag aac tgc ccg tac agc atc ctg gag ata aca 934
Ser Gly Thr Lys Lys Glu Asn Cys Pro Tyr Ser Ile Leu Glu Ile Thr
                100                      105                      110

tca gta gaa atc gga gtt gtt gcc gtc aaa gcc att aac agc aac tat 982
Ser Val Glu Ile Gly Val Val Ala Val Lys Ala Ile Asn Ser Asn Tyr
                115                      120                      125                      130

tac tta gcc atg aac aag aag ggg aaa ctc tat ggc tca aaa gaa ttt 1030
Tyr Leu Ala Met Asn Lys Lys Gly Lys Leu Tyr Gly Ser Lys Glu Phe
                    135                      140                      145

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aac aat gac tgt aag ctg aag gag agg ata gag gaa aat gga tac aat 1078
 Asn Asn Asp Cys Lys Leu Lys Glu Arg Ile Glu Glu Asn Gly Tyr Asn
 150 155 160

acc tat gca tca ttt aac tgg cag cat aat ggg agg caa atg tat gtg 1126
 Thr Tyr Ala Ser Phe Asn Trp Gln His Asn Gly Arg Gln Met Tyr Val
 165 170 175

gca ttg aat gga aaa gga gct cca agg aga gga cag aaa aca cga agg 1174
 Ala Leu Asn Gly Lys Gly Ala Pro Arg Arg Gly Gln Lys Thr Arg Arg
 180 185 190

aaa aac acc tct gct cac ttt ctt cca atg gtg gta cac tca 1216
 Lys Asn Thr Ser Ala His Phe Leu Pro Met Val Val His Ser
 195 200 205

tagaggaagg caccgtttgt ggatgcagta aaaccaatgg ctcttttgcc aagaatagtg 1276
 gatattcttc atgaagacag tagattgaaa ggcaaagaca cgttgcagat gtctgcttgc 1336
 ttaaaagaaa gccagccttt gaagggttttt gtattcactg ctgacatatg atgttctttt 1396
 aattagttct gtgtcatgtc ttataatcaa gatataggca gatcgaatgg gatagaagtt 1456
 attcccaagt gaaaaacatt gtggctgggt tttttgttgt tgttgtcaag tttttgtttt 1516
 taaacctctg agatagaact taaaggacat agaacaatct gttgaaagaa cgatcttcgg 1576
 gaaagttatt tatggaatac gaactcatat caaagacttc attgctcatt caagcctaata 1636
 gaatcaatga acagtaatac gtgcaagcat ttactggaaa gcacttgggt catatcatat 1696
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 taaacatggt agtgtgaaac tgttctaaca atacaaatag tatggtatgc ttgtgcattc 1816
 tgccttcac cctttctatt tctttctaag ttattttatt aataggatgt taaatatctt 1876
 ttgggggttt aaagagtatc tcagcagctg tcttctgatt tatcttttct ttttattcag 1936
 cacaccacat gcatgttcac gacaaagtgt ttttaaaact tggcgaacac ttcaaaaata 1996
 ggagttggga ttagggaagc agtatgagt cccgtgtgct atcagttgac ttaatttgca 2056
 cttctgcagt aataaccatc aacaataaat atggcaatgc tgtgccatgg cttgagtggag 2116
 agatgtctgc tatcatttga aaacatatat tactctcgag gcttctctgc tcaagaaata 2176
 gaccagaagg ccaaattctt ctctttcaat acatcagttt gcctccaaga atatactaaa 2236
 aaaaggaaaa ttaattgcta aatacattta aatagcctag cctcattatt tactcatgat 2296
 ttcttgccaa atgtcatggc ggtaaagagg ctgtccacat ctctaaaaac cctctgtaaa 2356
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 cccaggggct taaactgagc aaatcaaata tatactggta tatgtgtaac catatacaaa 2476
 aacctgttct agctgtatga tctagtcttt acaaaaccaa ataaaacttg ttttctgtaa 2536
 atttaaagag ctttacaagg ttccataatg taaccatatc aaaattcatt ttgtagagc 2596

acgtatagaa aagagtacat aagagtttac caatcatcat cacattgtat tccactaaat 2656
 aaatacataa gccttatttg cagtgtctgt agtgatttta aaaatgtaga aaaatactat 2716
 ttgttctaaa tacttttaag caataactat aatagtatat tgatgctgca gttttatctt 2776
 catatttctt gttttgaaaa agcattttat tgtttggaaca cagtattttg gtacaaaaaa 2836
 aaagactcac taaatgtgtc ttactaaagt ttaacctttg gaaatgctgg cgttctgtga 2896
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 attcttcaaa aaaactgtat ttcagaagaa acacatttga ggcaactgtct tttggcttat 3076
 agtttaaatt gcatttcac atactttgct tccaacttgc tttttggcaa atgagattat 3136
 aaaaatgttt aatttttgtg gttggaatct ggatgttaaa atttaattgg taactcagtc 3196
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 aaataataat ggcaactgac acatagacat agaccacca caacctaaat taaatgtttg 3316
 gtaagacaaa tacacatttg atgaccacag taacagcaaa cagggcacia actggattct 3376
 tatttcacat agacatttag attactaaag agggctatgt gtaaacagtc atcattatag 3436
 tactcaagac actaaaacag cttctagcca aatataataa agcttgcaga ggccaaaaat 3496
 agaaaacatc tcccctgtct ctcccacatt tccttcacag aaagacaaaa aacctgcctg 3556
 gtgcagtagc tcacacctgt aatcccagca gtttgggaga ctgtgggaag atggcttgag 3616
 tccaggagtt ctagacaggc ctgagaaacc tagtgagaca tccttctctt aaacaaaaca 3676
 aaacaaaaca aatgtagcca tgcgtggttg catatacctg tggcccaac tactcaggag 3736
 gctgaaacgg aaggatctct tgggccccag gagtttgagg ctgcagttag ctataatctt 3796
 gccattgcac tccagcctgg gtgaaaaaga gccagaaaga aaggaaagag agaaaagaga 3856
 aaagaaagag agaaaagaca gaaagacagg aaggaaggaa ggaaggaagg aaggaaggaa 3916
 ggaagcaagg aaagaaggaa ggaaggaaag aaggaggga aggaaggaga gagaaagaaa 3976
 gattgttttg taaggagtaa tgacattctc ttgcatttaa aagtggcata tttgcttgaa 4036
 atggaaatag aattctgggc ctttttgcaa ctactgaaga aaaaaaaaag cagtttcagc 4096
 cctgaatgtt gtagatttga aaaaaaaaaa aaaaaaactc gagggggggc ccgtacccaa 4156
 ttcgccttat agtgagtcgt a 4177

<210> 24

<211> 208

<212> PRT

<213> Homo sapiens

<400> 24

Met Trp Lys Trp Ile Leu Thr His Cys Ala Ser Ala Phe Pro His Leu

1	5	10	15
Pro Gly Cys Cys Cys Cys Cys Phe Leu Leu Leu Phe Leu Val Ser Ser	20	25	30
Val Pro Val Thr Cys Gln Ala Leu Gly Gln Asp Met Val Ser Pro Glu	35	40	45
Ala Thr Asn Ser Ser Ser Ser Ser Phe Ser Ser Pro Ser Ser Ala Gly	50	55	60
Arg His Val Arg Ser Tyr Asn His Leu Gln Gly Asp Val Arg Trp Arg	65	70	75
Lys Leu Phe Ser Phe Thr Lys Tyr Phe Leu Lys Ile Glu Lys Asn Gly	85	90	95
Lys Val Ser Gly Thr Lys Lys Glu Asn Cys Pro Tyr Ser Ile Leu Glu	100	105	110
Ile Thr Ser Val Glu Ile Gly Val Val Ala Val Lys Ala Ile Asn Ser	115	120	125
Asn Tyr Tyr Leu Ala Met Asn Lys Lys Gly Lys Leu Tyr Gly Ser Lys	130	135	140
Glu Phe Asn Asn Asp Cys Lys Leu Lys Glu Arg Ile Glu Glu Asn Gly	145	150	155
Tyr Asn Thr Tyr Ala Ser Phe Asn Trp Gln His Asn Gly Arg Gln Met	165	170	175
Tyr Val Ala Leu Asn Gly Lys Gly Ala Pro Arg Arg Gly Gln Lys Thr	180	185	190
Arg Arg Lys Asn Thr Ser Ala His Phe Leu Pro Met Val Val His Ser	195	200	205

<210> 25
 <211> 31
 <212> PRT
 <213> Homo sapiens

<400> 25
 Gly Gln Asp Met Val Ser Pro Glu Ala Thr Asn Ser Ser Ser Ser Ser
 1 5 10 15
 Phe Ser Ser Pro Ser Ser Ala Gly Arg His Val Arg Ser Tyr Asn
 20 25 30

<210> 26
 <211> 19
 <212> PRT
 <213> Homo sapiens

<400> 26
 Lys Ile Glu Lys Asn Gly Lys Val Ser Gly Thr Lys Lys Glu Asn Cys
 1 5 10 15

Pro Tyr Ser

<210> 27
 <211> 30
 <212> PRT
 <213> Homo sapiens

<400> 27
 Asn Lys Lys Gly Lys Leu Tyr Gly Ser Lys Glu Phe Asn Asn Asp Cys
 1 5 10 15
 Lys Leu Lys Glu Arg Ile Glu Glu Asn Gly Tyr Asn Thr Tyr
 20 25 30

<210> 28
 <211> 19
 <212> PRT
 <213> Homo sapiens

<400> 28
 Asn Gly Lys Gly Ala Pro Arg Arg Gly Gln Lys Thr Arg Arg Lys Asn
 1 5 10 15

Thr Ser Ala

<210> 29
 <211> 555
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> CDS
 <222> (1)..(552)

<220>
 <223> Description of Artificial Sequence: pQE60-Cys37
 construct

<400> 29
 atg aga gga teg cat cac cat cac cat cac gga tcc tgc cag gct ctg 48
 Met Arg Gly Ser His His His His His His Gly Ser Cys Gln Ala Leu
 1 5 10 15
 ggt cag gac atg gtt tct ccg gaa gct acc aac tct tcc tct tcc tct 96
 Gly Gln Asp Met Val Ser Pro Glu Ala Thr Asn Ser Ser Ser Ser Ser
 20 25 30
 ttc tct tcc ccg tct tcc gct ggt cgt cac gtt cgt tct tac aac cac 144
 Phe Ser Ser Pro Ser Ser Ala Gly Arg His Val Arg Ser Tyr Asn His
 35 40 45
 ctg cag ggt gac gtt cgt tgg cgt aaa ctg ttc tct ttc acc aaa tac 192
 Leu Gln Gly Asp Val Arg Trp Arg Lys Leu Phe Ser Phe Thr Lys Tyr
 50 55 60
 ttc ctg aaa atc gaa aaa aac ggt aaa gtt tct ggg acc aag aag gag 240
 Phe Leu Lys Ile Glu Lys Asn Gly Lys Val Ser Gly Thr Lys Lys Glu

65	70	75	80	
aac tgc ccg tac agc atc ctg gag ata aca tca gta gaa atc gga gtt				288
Asn Cys Pro Tyr Ser Ile Leu Glu Ile Thr Ser Val Glu Ile Gly Val				
	85	90	95	
gtt gcc gtc aaa gcc att aac agc aac tat tac tta gcc atg aac aag				336
Val Ala Val Lys Ala Ile Asn Ser Asn Tyr Tyr Leu Ala Met Asn Lys				
	100	105	110	
aag ggg aaa ctc tat ggc tca aaa gaa ttt aac aat gac tgt aag ctg				384
Lys Gly Lys Leu Tyr Gly Ser Lys Glu Phe Asn Asn Asp Cys Lys Leu				
	115	120	125	
aag gag agg ata gag gaa aat gga tac aat acc tat gca tca ttt aac				432
Lys Glu Arg Ile Glu Glu Asn Gly Tyr Asn Thr Tyr Ala Ser Phe Asn				
	130	135	140	
tgg cag cat aat ggg agg caa atg tat gtg gca ttg aat gga aaa gga				480
Trp Gln His Asn Gly Arg Gln Met Tyr Val Ala Leu Asn Gly Lys Gly				
	145	150	155	160
gct cca agg aga gga cag aaa aca cga agg aaa aac acc tct gct cac				528
Ala Pro Arg Arg Gly Gln Lys Thr Arg Arg Lys Asn Thr Ser Ala His				
	165	170	175	
ttt ctt cca atg gtg gta cac tca tag				555
Phe Leu Pro Met Val Val His Ser				
	180			

<210> 30

<211> 184

<212> PRT

<213> Artificial Sequence

<223> Description of Artificial Sequence: pQE60-Cys37
construct

<400> 30

Met Arg Gly Ser His His His His His His Gly Ser Cys Gln Ala Leu																			
1				5						10									15

Gly Gln Asp Met Val Ser Pro Glu Ala Thr Asn Ser Ser Ser Ser Ser																			
			20						25									30	

Phe Ser Ser Pro Ser Ser Ala Gly Arg His Val Arg Ser Tyr Asn His																			
			35					40						45					

Leu Gln Gly Asp Val Arg Trp Arg Lys Leu Phe Ser Phe Thr Lys Tyr																			
			50				55							60					

Phe Leu Lys Ile Glu Lys Asn Gly Lys Val Ser Gly Thr Lys Lys Glu																			
			65			70				75									80

Asn Cys Pro Tyr Ser Ile Leu Glu Ile Thr Ser Val Glu Ile Gly Val																			
				85					90									95	

Val Ala Val Lys Ala Ile Asn Ser Asn Tyr Tyr Leu Ala Met Asn Lys																			
			100					105									110		

Lys Gly Lys Leu Tyr Gly Ser Lys Glu Phe Asn Asn Asp Cys Lys Leu																			
			115					120						125					

Lys	Glu	Arg	Ile	Glu	Glu	Asn	Gly	Tyr	Asn	Thr	Tyr	Ala	Ser	Phe	Asn
130						135					140				
Trp	Gln	His	Asn	Gly	Arg	Gln	Met	Tyr	Val	Ala	Leu	Asn	Gly	Lys	Gly
145					150					155					160
Ala	Pro	Arg	Arg	Gly	Gln	Lys	Thr	Arg	Arg	Lys	Asn	Thr	Ser	Ala	His
				165					170					175	
Phe	Leu	Pro	Met	Val	Val	His	Ser								
			180												

<210> 31
 <211> 84
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: synthetic
 primer

<400> 31
 atgtggaaat ggatactgac ccaactgcgct tctgctttcc cgcacctgcc gggttgctgc 60
 tgctgctgct tctgctgct gttc 84

<210> 32
 <211> 82
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: synthetic
 primer

<400> 32
 ccggagaaac catgtcctga cccagagcct ggcaggtaac cggaacagaa gaaaccagga 60
 acagcagcag gaagcagcag ca 82

<210> 33
 <211> 80
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: synthetic
 primer

<400> 33
 gggtcaggac atggtttctc cggaagctac caactcttct tcttcttctt tctcttctcc 60
 gtcttctgct ggtcgtcacg 80

<210> 34
 <211> 81
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic
primer

<400> 34
ggtgaaagag aacagtttac gccaacgaac gtcaccctgc aggtggttgt aagaacgaac 60
gtgacgacca gcagaagacg g 81

<210> 35
<211> 75
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic
primer

<400> 35
cgttggcgta aactgttctc ttccacaaa tacttctga aaatcgaaaa aaacggtaaa 60
gtttctggga ccaa 75

<210> 36
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic
primer

<400> 36
tttggtccca gaaactttac cgtttttttc gattttcag 39

<210> 37
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic
primer

<400> 37
aaaggatcca tgtggaaatg gatactgacc cactgc 36

<210> 38
<211> 627
<212> DNA
<213> Escherichia coli

<220>
<221> CDS
<222> (1)..(627)

<400> 38
atg tgg aaa tgg ata ctg acc cac tgc gct tct gct ttc ccg cac ctg 48
Met Trp Lys Trp Ile Leu Thr His Cys Ala Ser Ala Phe Pro His Leu
1 5 10 15

ccg ggt tgc tgc tgc tgc tgc ttc ctg ctg ctg ttc ctg gtt tct tct	96
Pro Gly Cys Cys Cys Cys Cys Phe Leu Leu Leu Phe Leu Val Ser Ser	
20 25 30	
gtt ccg gtt acc tgc cag gct ctg ggt cag gac atg gtt tct ccg gaa	144
Val Pro Val Thr Cys Gln Ala Leu Gly Gln Asp Met Val Ser Pro Glu	
35 40 45	
gct acc aac tct tcc tct tcc tct ttc tct tcc ccg act tcc gct ggt	192
Ala Thr Asn Ser Ser Ser Ser Ser Phe Ser Ser Pro Thr Ser Ala Gly	
50 55 60	
cgt cac gtt cgt tct tac aac cac ctg cag ggt gac gtt cgt tgg cgt	240
Arg His Val Arg Ser Tyr Asn His Leu Gln Gly Asp Val Arg Trp Arg	
65 70 75 80	
aaa ctg ttc tct ttc acc aaa tac ttc ctg aaa atc gaa aaa aac ggt	288
Lys Leu Phe Ser Phe Thr Lys Tyr Phe Leu Lys Ile Glu Lys Asn Gly	
85 90 95	
aaa gtt tct ggg acc aag aag gag aac tgc ccg tac agc atc ctg gag	336
Lys Val Ser Gly Thr Lys Lys Glu Asn Cys Pro Tyr Ser Ile Leu Glu	
100 105 110	
ata aca tca gta gaa atc gga gtt gtt gcc gtc aaa gcc att aac agc	384
Ile Thr Ser Val Glu Ile Gly Val Val Ala Val Lys Ala Ile Asn Ser	
115 120 125	
aac tat tac tta gcc atg aac aag aag ggg aaa ctc tat ggc tca aaa	432
Asn Tyr Tyr Leu Ala Met Asn Lys Lys Gly Lys Leu Tyr Gly Ser Lys	
130 135 140	
gaa ttt aac aat gac tgt aag ctg aag gag agg ata gag gaa aat gga	480
Glu Phe Asn Asn Asp Cys Lys Leu Lys Glu Arg Ile Glu Glu Asn Gly	
145 150 155 160	
tac aat acc tat gca tca ttt aac tgg cag cat aat ggg agg caa atg	528
Tyr Asn Thr Tyr Ala Ser Phe Asn Trp Gln His Asn Gly Arg Gln Met	
165 170 175	
tat gtg gca ttg aat gga aaa gga gct cca agg aga gga cag aaa aca	576
Tyr Val Ala Leu Asn Gly Lys Gly Ala Pro Arg Arg Gly Gln Lys Thr	
180 185 190	
cga agg aaa aac acc tct gct cac ttt ctt cca atg gtg gta cac tca	624
Arg Arg Lys Asn Thr Ser Ala His Phe Leu Pro Met Val Val His Ser	
195 200 205	
tag	627

<210> 39
 <211> 208
 <212> PRT
 <213> Escherichia coli

<400> 39
 Met Trp Lys Trp Ile Leu Thr His Cys Ala Ser Ala Phe Pro His Leu
 1 5 10 15
 Pro Gly Cys Cys Cys Cys Phe Leu Leu Phe Leu Val Ser Ser
 20 25 30

Val	Pro	Val	Thr	Cys	Gln	Ala	Leu	Gly	Gln	Asp	Met	Val	Ser	Pro	Glu
		35					40					45			
Ala	Thr	Asn	Ser	Ser	Ser	Ser	Ser	Phe	Ser	Ser	Pro	Thr	Ser	Ala	Gly
	50					55					60				
Arg	His	Val	Arg	Ser	Tyr	Asn	His	Leu	Gln	Gly	Asp	Val	Arg	Trp	Arg
	65				70					75				80	
Lys	Leu	Phe	Ser	Phe	Thr	Lys	Tyr	Phe	Leu	Lys	Ile	Glu	Lys	Asn	Gly
				85					90					95	
Lys	Val	Ser	Gly	Thr	Lys	Lys	Glu	Asn	Cys	Pro	Tyr	Ser	Ile	Leu	Glu
			100					105					110		
Ile	Thr	Ser	Val	Glu	Ile	Gly	Val	Val	Ala	Val	Lys	Ala	Ile	Asn	Ser
		115					120					125			
Asn	Tyr	Tyr	Leu	Ala	Met	Asn	Lys	Lys	Gly	Lys	Leu	Tyr	Gly	Ser	Lys
	130					135					140				
Glu	Phe	Asn	Asn	Asp	Cys	Lys	Leu	Lys	Glu	Arg	Ile	Glu	Glu	Asn	Gly
	145				150					155					160
Tyr	Asn	Thr	Tyr	Ala	Ser	Phe	Asn	Trp	Gln	His	Asn	Gly	Arg	Gln	Met
				165					170					175	
Tyr	Val	Ala	Leu	Asn	Gly	Lys	Gly	Ala	Pro	Arg	Arg	Gly	Gln	Lys	Thr
			180					185					190		
Arg	Arg	Lys	Asn	Thr	Ser	Ala	His	Phe	Leu	Pro	Met	Val	Val	His	Ser
		195					200					205			

<210> 40
 <211> 38
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

<400> 40
 ttctcatgact tgtcaagctc tgggtcaaga tatggttc

38

<210> 41
 <211> 28
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

<400> 41
 gcccaagctt ccacaaacgt tgccttcc

28

<210> 42
 <211> 525
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)..(522)

<400> 42
 atg acc tgc cag gct ctg ggt cag gac atg gtt tct ccg gaa gct acc
 Met Thr Cys Gln Ala Leu Gly Gln Asp Met Val Ser Pro Glu Ala Thr
 1 5 10 15

48

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aac tct tcc tct tcc tct ttc tct tcc ccg tct tcc gct ggt cgt cac    96
Asn Ser Ser Ser Ser Ser Ser Phe Ser Ser Pro Ser Ser Ala Gly Arg His
                20                      25                      30

ggt cgt tct tac aac cac ctg cag ggt gac gtt cgt tgg cgt aaa ctg    144
Val Arg Ser Tyr Asn His Leu Gln Gly Asp Val Arg Trp Arg Lys Leu
                35                      40                      45

ttc tct ttc acc aaa tac ttc ctg aaa atc gaa aaa aac ggt aaa gtt    192
Phe Ser Phe Thr Lys Tyr Phe Leu Lys Ile Glu Lys Asn Gly Lys Val
                50                      55                      60

tct ggg acc aag aag gag aac tgc ccg tac agc atc ctg gag ata aca    240
Ser Gly Thr Lys Lys Glu Asn Cys Pro Tyr Ser Ile Leu Glu Ile Thr
                65                      70                      75                      80

tca gta gaa atc gga gtt gtt gcc gtc aaa gcc att aac agc aac tat    288
Ser Val Glu Ile Gly Val Val Ala Val Lys Ala Ile Asn Ser Asn Tyr
                85                      90                      95

tac tta gcc atg aac aag aag ggg aaa ctc tat ggc tca aaa gaa ttt    336
Tyr Leu Ala Met Asn Lys Lys Gly Lys Leu Tyr Gly Ser Lys Glu Phe
                100                      105                      110

aac aat gac tgt aag ctg aag gag agg ata gag gaa aat gga tac aat    384
Asn Asn Asp Cys Lys Leu Lys Glu Arg Ile Glu Glu Asn Gly Tyr Asn
                115                      120                      125

acc tat gca tca ttt aac tgg cag cat aat ggg agg caa atg tat gtg    432
Thr Tyr Ala Ser Phe Asn Trp Gln His Asn Gly Arg Gln Met Tyr Val
                130                      135                      140

gca ttg aat gga aaa gga gct cca agg aga gga cag aaa aca cga agg    480
Ala Leu Asn Gly Lys Gly Ala Pro Arg Arg Gly Gln Lys Thr Arg Arg
                145                      150                      155                      160

aaa aac acc tct gct cac ttt ctt cca atg gtg gta cac tca tag    525
Lys Asn Thr Ser Ala His Phe Leu Pro Met Val Val His Ser
                165                      170

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<210> 43
 <211> 174
 <212> PRT
 <213> Escherichia coli

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<400> 43
Met Thr Cys Gln Ala Leu Gly Gln Asp Met Val Ser Pro Glu Ala Thr
  1                5                10                15

Asn Ser Ser Ser Ser Ser Phe Ser Ser Pro Ser Ser Ala Gly Arg His
                20                      25                      30

Val Arg Ser Tyr Asn His Leu Gln Gly Asp Val Arg Trp Arg Lys Leu
                35                      40                      45

Phe Ser Phe Thr Lys Tyr Phe Leu Lys Ile Glu Lys Asn Gly Lys Val
                50                      55                      60

Ser Gly Thr Lys Lys Glu Asn Cys Pro Tyr Ser Ile Leu Glu Ile Thr
                65                      70                      75                      80

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Ser Val Glu Ile Gly Val Val Ala Val Lys Ala Ile Asn Ser Asn Tyr
85 90 95
Tyr Leu Ala Met Asn Lys Lys Gly Lys Leu Tyr Gly Ser Lys Glu Phe
100 105 110
Asn Asn Asp Cys Lys Leu Lys Glu Arg Ile Glu Glu Asn Gly Tyr Asn
115 120 125
Thr Tyr Ala Ser Phe Asn Trp Gln His Asn Gly Arg Gln Met Tyr Val
130 135 140
Ala Leu Asn Gly Lys Gly Ala Pro Arg Arg Gly Gln Lys Thr Arg Arg
145 150 155 160
Lys Asn Thr Ser Ala His Phe Leu Pro Met Val Val His Ser
165 170

<210> 44
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic
primer

<400> 44
tcagtgaatt cattaaagag gagaaattaa tcatgacttg ccagg 45

<210> 45
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic
primer

<400> 45
tcatgacttg ccaggcactg ggtcaagaca tggtttcccc ggaagcta 48

<210> 46
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic
primer

<400> 46
gcttcagcag cccatctagc gcaggtcgctc acgttcgctc ttacaacc 48

<210> 47
<211> 48
<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic primer

<400> 47

gttcggtggc gcaaactggt cagctttacc aagtacttcc tgaaaatc

48

<210> 48

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic primer

<400> 48

tcgaaaaaaaa cggtaaagtt tctgggac

28

<210> 49

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic primer

<400> 49

gatgggctgc tgaagctaga gctggagctg ttggtagctt ccggggaa

48

<210> 50

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic primer

<400> 50

aacagtttgc gccaacgaac atcacctgt aagtggttgt aagag

45

<210> 51

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic primer

<400> 51

ttcttgggcc cagaaacttt accgtttttt tcgattttca ggaagta

47

<210> 52
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: synthetic
 primer

<400> 52
 ttcttggtcc cagaaacttt accg 24

<210> 53
 <211> 45
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: synthetic
 primer

<400> 53
 agatcaggct tctattatta tgagtgtacc accattggaa gaaag 45

<210> 54
 <211> 525
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)..(522)

<400> 54
 atg act tgc cag gca ctg ggt caa gac atg gtt tcc ccg gaa gct acc 48
 Met Thr Cys Gln Ala Leu Gly Gln Asp Met Val Ser Pro Glu Ala Thr
 1 5 10 15

aac agc tcc agc tct agc ttc agc agc cca tct agc gca ggt cgt cac 96
 Asn Ser Ser Ser Ser Phe Ser Ser Pro Ser Ser Ala Gly Arg His
 20 25 30

gtt cgc tct tac aac cac tta cag ggt gat gtt cgt tgg cgc aaa ctg 144
 Val Arg Ser Tyr Asn His Leu Gln Gly Asp Val Arg Trp Arg Lys Leu
 35 40 45

ttc agc ttt acc aag tac ttc ctg aaa atc gaa aaa aac ggt aaa gtt 192
 Phe Ser Phe Thr Lys Tyr Phe Leu Lys Ile Glu Lys Asn Gly Lys Val
 50 55 60

tct ggg acc aag aag gag aac tgc ccg tac agc atc ctg gag ata aca 240
 Ser Gly Thr Lys Lys Glu Asn Cys Pro Tyr Ser Ile Leu Glu Ile Thr
 65 70 75 80

tca gta gaa atc gga gtt gtt gcc gtc aaa gcc att aac agc aac tat 288
 Ser Val Glu Ile Gly Val Val Ala Val Lys Ala Ile Asn Ser Asn Tyr
 85 90 95

tac tta gcc atg aac aag aag ggg aaa ctc tat ggc tca aaa gaa ttt 336
 Tyr Leu Ala Met Asn Lys Lys Gly Lys Leu Tyr Gly Ser Lys Glu Phe

100										105										110										
aac	aat	gac	tgt	aag	ctg	aag	gag	agg	ata	gag	gaa	aat	gga	tac	aat	384														
Asn	Asn	Asp	Cys	Lys	Leu	Lys	Glu	Arg	Ile	Glu	Glu	Asn	Gly	Tyr	Asn															
		115					120					125																		
acc	tat	gca	tca	ttt	aac	tgg	cag	cat	aat	ggg	agg	caa	atg	tat	gtg	432														
Thr	Tyr	Ala	Ser	Phe	Asn	Trp	Gln	His	Asn	Gly	Arg	Gln	Met	Tyr	Val															
	130					135					140																			
gca	ttg	aat	gga	aaa	gga	gct	cca	agg	aga	gga	cag	aaa	aca	cga	agg	480														
Ala	Leu	Asn	Gly	Lys	Gly	Ala	Pro	Arg	Arg	Gly	Gln	Lys	Thr	Arg	Arg															
145					150					155					160															
aaa	aac	acc	tct	gct	cac	ttt	ctt	cca	atg	gtg	gta	cac	tca	tag		525														
Lys	Asn	Thr	Ser	Ala	His	Phe	Leu	Pro	Met	Val	Val	His	Ser																	
				165					170																					

<210> 55
 <211> 174
 <212> PRT
 <213> Escherichia coli

<400> 55
 Met Thr Cys Gln Ala Leu Gly Gln Asp Met Val Ser Pro Glu Ala Thr
 1 5 10 15
 Asn Ser Ser Ser Ser Ser Phe Ser Ser Pro Ser Ser Ala Gly Arg His
 20 25 30
 Val Arg Ser Tyr Asn His Leu Gln Gly Asp Val Arg Trp Arg Lys Leu
 35 40 45
 Phe Ser Phe Thr Lys Tyr Phe Leu Lys Ile Glu Lys Asn Gly Lys Val
 50 55 60
 Ser Gly Thr Lys Lys Glu Asn Cys Pro Tyr Ser Ile Leu Glu Ile Thr
 65 70 75 80
 Ser Val Glu Ile Gly Val Val Ala Val Lys Ala Ile Asn Ser Asn Tyr
 85 90 95
 Tyr Leu Ala Met Asn Lys Lys Gly Lys Leu Tyr Gly Ser Lys Glu Phe
 100 105 110
 Asn Asn Asp Cys Lys Leu Lys Glu Arg Ile Glu Glu Asn Gly Tyr Asn
 115 120 125
 Thr Tyr Ala Ser Phe Asn Trp Gln His Asn Gly Arg Gln Met Tyr Val
 130 135 140
 Ala Leu Asn Gly Lys Gly Ala Pro Arg Arg Gly Gln Lys Thr Arg Arg
 145 150 155 160
 Lys Asn Thr Ser Ala His Phe Leu Pro Met Val Val His Ser
 165 170

<210> 56
 <211> 35

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 56
ggaccctcat gacctgccag gctctgggtc aggac 35

<210> 57
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 57
ggacagccat ggctggtcgt cacgttcg 28

<210> 58
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 58
ggacagccat gggtcgttgg cgtaaactg 29

<210> 59
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 59
ggacagccat ggaaaaaac ggtaaagttt c 31

<210> 60
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 60
ggaccccat ggagaactgc ccgtagagc 29

<210> 61
<211> 32
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 61

ggacccccat ggtcaaagcc attaacagca ac 32

<210> 62

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 62

ggacccccat ggggaaactc tatggctcaa aag 33

<210> 63

<211> 37

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 63

ctgcccaagc ttattatgag tgtaccacca ttggaag 37

<210> 64

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 64

ctgcccaagc ttattacttc agcttacagt cattgt 36

<210> 65

<211> 525

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(522)

<400> 65

atg acc tgc cag gct ctg ggt cag gac atg gtt tct ccg gaa gct acc 48
Met Thr Cys Gln Ala Leu Gly Gln Asp Met Val Ser Pro Glu Ala Thr
1 5 10 15

aac tct tcc tct tcc tct ttc tct tcc ccg tct tcc gct ggt cgt cac 96
Asn Ser Ser Ser Ser Ser Phe Ser Ser Pro Ser Ser Ala Gly Arg His
20 25 30

ggt cgt tct tac aac cac ctg cag ggt gac gtt cgt tgg cgt aaa ctg 144

Val	Arg	Ser	Tyr	Asn	His	Leu	Gln	Gly	Asp	Val	Arg	Trp	Arg	Lys	Leu		
		35					40					45					
ttc	tct	ttc	acc	aaa	tac	ttc	ctg	aaa	atc	gaa	aaa	aac	ggt	aaa	gtt	192	
Phe	Ser	Phe	Thr	Lys	Tyr	Phe	Leu	Lys	Ile	Glu	Lys	Asn	Gly	Lys	Val		
	50					55					60						
tct	ggg	acc	aag	aag	gag	aac	tgc	ccg	tac	agc	atc	ctg	gag	ata	aca	240	
Ser	Gly	Thr	Lys	Lys	Glu	Asn	Cys	Pro	Tyr	Ser	Ile	Leu	Glu	Ile	Thr		
	65				70					75					80		
tca	gta	gaa	atc	gga	gtt	gtt	gcc	gtc	aaa	gcc	att	aac	agc	aac	tat	288	
Ser	Val	Glu	Ile	Gly	Val	Val	Ala	Val	Lys	Ala	Ile	Asn	Ser	Asn	Tyr		
				85					90					95			
tac	tta	gcc	atg	aac	aag	aag	ggg	aaa	ctc	tat	ggc	tca	aaa	gaa	ttt	336	
Tyr	Leu	Ala	Met	Asn	Lys	Lys	Gly	Lys	Leu	Tyr	Gly	Ser	Lys	Glu	Phe		
			100				105						110				
aac	aat	gac	tgt	aag	ctg	aag	gag	agg	ata	gag	gaa	aat	gga	tac	aat	384	
Asn	Asn	Asp	Cys	Lys	Leu	Lys	Glu	Arg	Ile	Glu	Glu	Asn	Gly	Tyr	Asn		
		115					120					125					
acc	tat	gca	tca	ttt	aac	tgg	cag	cat	aat	ggg	agg	caa	atg	tat	gtg	432	
Thr	Tyr	Ala	Ser	Phe	Asn	Trp	Gln	His	Asn	Gly	Arg	Gln	Met	Tyr	Val		
	130					135					140						
gca	ttg	aat	gga	aaa	gga	gct	cca	agg	aga	gga	cag	aaa	aca	cga	agg	480	
Ala	Leu	Asn	Gly	Lys	Gly	Ala	Pro	Arg	Arg	Gly	Gln	Lys	Thr	Arg	Arg		
	145				150					155					160		
aaa	aac	acc	tct	gct	cac	ttt	ctt	cca	atg	gtg	gta	cac	tca	tag		525	
Lys	Asn	Thr	Ser	Ala	His	Phe	Leu	Pro	Met	Val	Val	His	Ser				
				165					170								

<210> 66
 <211> 174
 <212> PRT
 <213> Homo sapiens

<400> 66
 Met Thr Cys Gln Ala Leu Gly Gln Asp Met Val Ser Pro Glu Ala Thr
 1 5 10 15
 Asn Ser Ser Ser Ser Ser Phe Ser Ser Pro Ser Ser Ala Gly Arg His
 20 25 30
 Val Arg Ser Tyr Asn His Leu Gln Gly Asp Val Arg Trp Arg Lys Leu
 35 40 45
 Phe Ser Phe Thr Lys Tyr Phe Leu Lys Ile Glu Lys Asn Gly Lys Val
 50 55 60
 Ser Gly Thr Lys Lys Glu Asn Cys Pro Tyr Ser Ile Leu Glu Ile Thr
 65 70 75 80
 Ser Val Glu Ile Gly Val Val Ala Val Lys Ala Ile Asn Ser Asn Tyr
 85 90 95
 Tyr Leu Ala Met Asn Lys Lys Gly Lys Leu Tyr Gly Ser Lys Glu Phe
 100 105 110

Asn Asn Asp Cys Lys Leu Lys Glu Arg Ile Glu Glu Asn Gly Tyr Asn
 115 120 125
 Thr Tyr Ala Ser Phe Asn Trp Gln His Asn Gly Arg Gln Met Tyr Val
 130 135 140
 Ala Leu Asn Gly Lys Gly Ala Pro Arg Arg Gly Gln Lys Thr Arg Arg
 145 150 155 160
 Lys Asn Thr Ser Ala His Phe Leu Pro Met Val Val His Ser
 165 170

<210> 67
 <211> 444
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(444)

<400> 67
 atg gct ggt cgt cac gtt cgt tct tac aac cac ctg cag ggt gac gtt 48
 Met Ala Gly Arg His Val Arg Ser Tyr Asn His Leu Gln Gly Asp Val
 1 5 10 15
 cgt tgg cgt aaa ctg ttc tct ttc acc aaa tac ttc ctg aaa atc gaa 96
 Arg Trp Arg Lys Leu Phe Ser Phe Thr Lys Tyr Phe Leu Lys Ile Glu
 20 25 30
 aaa aac ggt aaa gtt tct ggg acc aag aag gag aac tgc ccg tac agc 144
 Lys Asn Gly Lys Val Ser Gly Thr Lys Lys Glu Asn Cys Pro Tyr Ser
 35 40 45
 atc ctg gag ata aca tca gta gaa atc gga gtt gtt gcc gtc aaa gcc 192
 Ile Leu Glu Ile Thr Ser Val Glu Ile Gly Val Val Ala Val Lys Ala
 50 55 60
 att aac agc aac tat tac tta gcc atg aac aag aag ggg aaa ctc tat 240
 Ile Asn Ser Asn Tyr Tyr Leu Ala Met Asn Lys Lys Gly Lys Leu Tyr
 65 70 75 80
 ggc tca aaa gaa ttt aac aat gac tgt aag ctg aag gag agg ata gag 288
 Gly Ser Lys Glu Phe Asn Asn Asp Cys Lys Leu Lys Glu Arg Ile Glu
 85 90 95
 gaa aat gga tac aat acc tat gca tca ttt aac tgg cag cat aat ggg 336
 Glu Asn Gly Tyr Asn Thr Tyr Ala Ser Phe Asn Trp Gln His Asn Gly
 100 105 110
 agg caa atg tat gtg gca ttg aat gga aaa gga gct cca agg aga gga 384
 Arg Gln Met Tyr Val Ala Leu Asn Gly Lys Gly Ala Pro Arg Arg Gly
 115 120 125
 cag aaa aca cga agg aaa aac acc tct gct cac ttt ctt cca atg gtg 432
 Gln Lys Thr Arg Arg Lys Asn Thr Ser Ala His Phe Leu Pro Met Val
 130 135 140
 gta cac tca tag 444
 Val His Ser

145

<210> 68
<211> 147
<212> PRT
<213> Homo sapiens

<400> 68
Met Ala Gly Arg His Val Arg Ser Tyr Asn His Leu Gln Gly Asp Val
1 5 10 15
Arg Trp Arg Lys Leu Phe Ser Phe Thr Lys Tyr Phe Leu Lys Ile Glu
20 25 30
Lys Asn Gly Lys Val Ser Gly Thr Lys Lys Glu Asn Cys Pro Tyr Ser
35 40 45
Ile Leu Glu Ile Thr Ser Val Glu Ile Gly Val Val Ala Val Lys Ala
50 55 60
Ile Asn Ser Asn Tyr Tyr Leu Ala Met Asn Lys Lys Gly Lys Leu Tyr
65 70 75 80
Gly Ser Lys Glu Phe Asn Asn Asp Cys Lys Leu Lys Glu Arg Ile Glu
85 90 95
Glu Asn Gly Tyr Asn Thr Tyr Ala Ser Phe Asn Trp Gln His Asn Gly
100 105 110
Arg Gln Met Tyr Val Ala Leu Asn Gly Lys Gly Ala Pro Arg Arg Gly
115 120 125
Gln Lys Thr Arg Arg Lys Asn Thr Ser Ala His Phe Leu Pro Met Val
130 135 140
Val His Ser
145

<210> 69
<211> 402
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(402)

<400> 69
atg gtt cgt tgg cgt aaa ctg ttc tct ttc acc aaa tac ttc ctg aaa 48
Met Val Arg Trp Arg Lys Leu Phe Ser Phe Thr Lys Tyr Phe Leu Lys
1 5 10 15
atc gaa aaa aac ggt aaa gtt tct ggg acc aag aag gag aac tgc ccg 96
Ile Glu Lys Asn Gly Lys Val Ser Gly Thr Lys Lys Glu Asn Cys Pro
20 25 30
tac agc atc ctg gag ata aca tca gta gaa atc gga gtt gtt gcc gtc 144
Tyr Ser Ile Leu Glu Ile Thr Ser Val Glu Ile Gly Val Val Ala Val
35 40 45
aaa gcc att aac agc aac tat tac tta gcc atg aac aag aag ggg aaa 192
Lys Ala Ile Asn Ser Asn Tyr Tyr Leu Ala Met Asn Lys Lys Gly Lys
50 55 60
ctc tat ggc tca aaa gaa ttt aac aat gac tgt aag ctg aag gag agg 240
Leu Tyr Gly Ser Lys Glu Phe Asn Asn Asp Cys Lys Leu Lys Glu Arg
65 70 75 80

ata gag gaa aat gga tac aat acc tat gca tca ttt aac tgg cag cat	288
Ile Glu Glu Asn Gly Tyr Asn Thr Tyr Ala Ser Phe Asn Trp Gln His	
85 90 95	
aat ggg agg caa atg tat gtg gca ttg aat gga aaa gga gct cca agg	336
Asn Gly Arg Gln Met Tyr Val Ala Leu Asn Gly Lys Gly Ala Pro Arg	
100 105 110	
aga gga cag aaa aca cga agg aaa aac acc tct gct cac ttt ctt cca	384
Arg Gly Gln Lys Thr Arg Arg Lys Asn Thr Ser Ala His Phe Leu Pro	
115 120 125	
atg gtg gta cac tca tag	402
Met Val Val His Ser	
130	

<210> 70
 <211> 133
 <212> PRT
 <213> Homo sapiens

<400> 70	
Met Val Arg Trp Arg Lys Leu Phe Ser Phe Thr Lys Tyr Phe Leu Lys	
1 5 10 15	
Ile Glu Lys Asn Gly Lys Val Ser Gly Thr Lys Lys Glu Asn Cys Pro	
20 25 30	
Tyr Ser Ile Leu Glu Ile Thr Ser Val Glu Ile Gly Val Val Ala Val	
35 40 45	
Lys Ala Ile Asn Ser Asn Tyr Tyr Leu Ala Met Asn Lys Lys Gly Lys	
50 55 60	
Leu Tyr Gly Ser Lys Glu Phe Asn Asn Asp Cys Lys Leu Lys Glu Arg	
65 70 75 80	
Ile Glu Glu Asn Gly Tyr Asn Thr Tyr Ala Ser Phe Asn Trp Gln His	
85 90 95	
Asn Gly Arg Gln Met Tyr Val Ala Leu Asn Gly Lys Gly Ala Pro Arg	
100 105 110	
Arg Gly Gln Lys Thr Arg Arg Lys Asn Thr Ser Ala His Phe Leu Pro	
115 120 125	
Met Val Val His Ser	
130	

<210> 71
 <211> 354
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(354)

<400> 71	
atg gaa aaa aac ggt aaa gtt tct ggg acc aag aag gag aac tgc ccg	48
Met Glu Lys Asn Gly Lys Val Ser Gly Thr Lys Lys Glu Asn Cys Pro	
1 5 10 15	
tac agc atc ctg gag ata aca tca gta gaa atc gga gtt gtt gcc gtc	96
Tyr Ser Ile Leu Glu Ile Thr Ser Val Glu Ile Gly Val Val Ala Val	
20 25 30	

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aaa gcc att aac agc aac tat tac tta gcc atg aac aag aag ggg aaa 144
Lys Ala Ile Asn Ser Asn Tyr Tyr Leu Ala Met Asn Lys Lys Gly Lys
      35                      40                      45

ctc tat ggc tca aaa gaa ttt aac aat gac tgt aag ctg aag gag agg 192
Leu Tyr Gly Ser Lys Glu Phe Asn Asn Asp Cys Lys Leu Lys Glu Arg
      50                      55                      60

ata gag gaa aat gga tac aat acc tat gca tca ttt aac tgg cag cat 240
Ile Glu Glu Asn Gly Tyr Asn Thr Tyr Ala Ser Phe Asn Trp Gln His
      65                      70                      75

aat ggg agg caa atg tat gtg gca ttg aat gga aaa gga gct cca agg 288
Asn Gly Arg Gln Met Tyr Val Ala Leu Asn Gly Lys Gly Ala Pro Arg
      85                      90                      95

aga gga cag aaa aca cga agg aaa aac acc tct gct cac ttt ctt cca 336
Arg Gly Gln Lys Thr Arg Arg Lys Asn Thr Ser Ala His Phe Leu Pro
      100                      105                      110

atg gtg gta cac tca tag 354
Met Val Val His Ser
      115

```

<210> 72
 <211> 117
 <212> PRT
 <213> Homo sapiens

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<400> 72
Met Glu Lys Asn Gly Lys Val Ser Gly Thr Lys Lys Glu Asn Cys Pro
  1          5          10          15
Tyr Ser Ile Leu Glu Ile Thr Ser Val Glu Ile Gly Val Val Ala Val
      20          25          30
Lys Ala Ile Asn Ser Asn Tyr Tyr Leu Ala Met Asn Lys Lys Gly Lys
      35          40          45
Leu Tyr Gly Ser Lys Glu Phe Asn Asn Asp Cys Lys Leu Lys Glu Arg
      50          55          60
Ile Glu Glu Asn Gly Tyr Asn Thr Tyr Ala Ser Phe Asn Trp Gln His
      65          70          75          80
Asn Gly Arg Gln Met Tyr Val Ala Leu Asn Gly Lys Gly Ala Pro Arg
      85          90          95
Arg Gly Gln Lys Thr Arg Arg Lys Asn Thr Ser Ala His Phe Leu Pro
      100          105          110
Met Val Val His Ser
      115

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<210> 73
 <211> 321
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(321)

```

<400> 73
atg gag aac tgc ccg tac agc atc ctg gag ata aca tca gta gaa atc 48
Met Glu Asn Cys Pro Tyr Ser Ile Leu Glu Ile Thr Ser Val Glu Ile

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1	5	10	15	
gga gtt gtt gcc gtc aaa gcc att aac agc aac tat tac tta gcc atg				96
Gly Val Val Ala Val Lys Ala Ile Asn Ser Asn Tyr Tyr Leu Ala Met	20	25	30	
aac aag aag ggg aaa ctc tat ggc tca aaa gaa ttt aac aat gac tgt				144
Asn Lys Lys Gly Lys Leu Tyr Gly Ser Lys Glu Phe Asn Asn Asp Cys	35	40	45	
aag ctg aag gag agg ata gag gaa aat gga tac aat acc tat gca tca				192
Lys Leu Lys Gly Arg Ile Glu Glu Asn Gly Tyr Asn Thr Tyr Ala Ser	50	55	60	
ttt aac tgg cag cat aat ggg agg caa atg tat gtg gca ttg aat gga				240
Phe Asn Trp Gln His Asn Gly Arg Gln Met Tyr Val Ala Leu Asn Gly	65	70	75	80
aaa gga gct cca agg aga gga cag aaa aca cga agg aaa aac acc tct				288
Lys Gly Ala Pro Arg Arg Gly Gln Lys Thr Arg Arg Lys Asn Thr Ser	85	90	95	
gct cac ttt ctt cca atg gtg gta cac tca tag				321
Ala His Phe Leu Pro Met Val Val His Ser	100	105		

<210> 74
 <211> 106
 <212> PRT
 <213> Homo sapiens

<400> 74
 Met Glu Asn Cys Pro Tyr Ser Ile Leu Glu Ile Thr Ser Val Glu Ile
 1 5 10 15
 Gly Val Val Ala Val Lys Ala Ile Asn Ser Asn Tyr Tyr Leu Ala Met
 20 25 30
 Asn Lys Lys Gly Lys Leu Tyr Gly Ser Lys Glu Phe Asn Asn Asp Cys
 35 40 45
 Lys Leu Lys Glu Arg Ile Glu Glu Asn Gly Tyr Asn Thr Tyr Ala Ser
 50 55 60
 Phe Asn Trp Gln His Asn Gly Arg Gln Met Tyr Val Ala Leu Asn Gly
 65 70 75 80
 Lys Gly Ala Pro Arg Arg Gly Gln Lys Thr Arg Arg Lys Asn Thr Ser
 85 90 95
 Ala His Phe Leu Pro Met Val Val His Ser
 100 105

<210> 75
 <211> 264
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(261)

<400> 75
 atg gtc aaa gcc att aac agc aac tat tac tta gcc atg aac aag aag 48
 Met Val Lys Ala Ile Asn Ser Asn Tyr Tyr Leu Ala Met Asn Lys Lys

1	5	10	15	
ggg aaa ctc tat ggc tca aaa gaa ttt aac aat gac tgt aag ctg aag				96
Gly Lys Leu Tyr	Gly Ser Lys Glu	Phe Asn Asn Asp Cys	Lys Leu Lys	
20		25	30	
gag agg ata gag gaa aat gga tac aat acc tat gca tca ttt aac tgg				144
Glu Arg Ile Glu Glu Asn Gly Tyr Asn Thr Tyr Ala Ser Phe Asn Trp				
35	40		45	
cag cat aat ggg agg caa atg tat gtg gca ttg aat gga aaa gga gct				192
Gln His Asn Gly Arg Gln Met Tyr Val Ala Leu Asn Gly Lys Gly Ala				
50	55		60	
cca agg aga gga cag aaa aca cga agg aaa aac acc tct gct cac ttt				240
Pro Arg Arg Gly Gln Lys Thr Arg Arg Lys Asn Thr Ser Ala His Phe				
65	70		75	80
ctt cca atg gtg gta cac tca tag				264
Leu Pro Met Val Val His Ser				
	85			

<210> 76
 <211> 87
 <212> PRT
 <213> Homo sapiens

<400> 76
 Met Val Lys Ala Ile Asn Ser Asn Tyr Tyr Leu Ala Met Asn Lys Lys
 1 5 10 15
 Gly Lys Leu Tyr Gly Ser Lys Glu Phe Asn Asn Asp Cys Lys Leu Lys
 20 25 30
 Glu Arg Ile Glu Glu Asn Gly Tyr Asn Thr Tyr Ala Ser Phe Asn Trp
 35 40 45
 Gln His Asn Gly Arg Gln Met Tyr Val Ala Leu Asn Gly Lys Gly Ala
 50 55 60
 Pro Arg Arg Gly Gln Lys Thr Arg Arg Lys Asn Thr Ser Ala His Phe
 65 70 75 80
 Leu Pro Met Val Val His Ser
 85

<210> 77
 <211> 219
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(219)

<400> 77
 atg ggg aaa ctc tat ggc tca aaa gaa ttt aac aat gac tgt aag ctg 48
 Met Gly Lys Leu Tyr Gly Ser Lys Glu Phe Asn Asn Asp Cys Lys Leu
 1 5 10 15

aag gag agg ata gag gaa aat gga tac aat acc tat gca tca ttt aac 96
 Lys Glu Arg Ile Glu Glu Asn Gly Tyr Asn Thr Tyr Ala Ser Phe Asn
 20 25 30

tgg cag cat aat ggg agg caa atg tat gtg gca ttg aat gga aaa gga 144
 Trp Gln His Asn Gly Arg Gln Met Tyr Val Ala Leu Asn Gly Lys Gly
 35 40 45

gct cca agg aga gga cag aaa aca cga agg aaa aac acc tct gct cac 192
 Ala Pro Arg Arg Gly Gln Lys Thr Arg Arg Lys Asn Thr Ser Ala His
 50 55 60

ttt ctt cca atg gtg gta cac tca tag 219
 Phe Leu Pro Met Val Val His Ser
 65 70

<210> 78
 <211> 72
 <212> PRT
 <213> Homo sapiens

<400> 78
 Met Gly Lys Leu Tyr Gly Ser Lys Glu Phe Asn Asn Asp Cys Lys Leu
 1 5 10 15
 Lys Glu Arg Ile Glu Glu Asn Gly Tyr Asn Thr Tyr Ala Ser Phe Asn
 20 25 30
 Trp Gln His Asn Gly Arg Gln Met Tyr Val Ala Leu Asn Gly Lys Gly
 35 40 45
 Ala Pro Arg Arg Gly Gln Lys Thr Arg Arg Lys Asn Thr Ser Ala His
 50 55 60
 Phe Leu Pro Met Val Val His Ser
 65 70

<210> 79
 <211> 357
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(357)

<400> 79
 atg acc tgc cag gct ctg ggt cag gac atg gtt tct ccg gaa gct acc 48
 Met Thr Cys Gln Ala Leu Gly Gln Asp Met Val Ser Pro Glu Ala Thr
 1 5 10 15

aac tct tcc tct tcc tct ttc tct tcc ccg tct tcc gct ggt cgt cac 96
 Asn Ser Ser Ser Ser Ser Phe Ser Ser Pro Ser Ser Ala Gly Arg His
 20 25 30

gtt cgt tct tac aac cac ctg cag ggt gac gtt cgt tgg cgt aaa ctg 144
 Val Arg Ser Tyr Asn His Leu Gln Gly Asp Val Arg Trp Arg Lys Leu
 35 40 45

ttc tct ttc acc aaa tac ttc ctg aaa atc gaa aaa aac ggt aaa gtt 192
 Phe Ser Phe Thr Lys Tyr Phe Leu Lys Ile Glu Lys Asn Gly Lys Val
 50 55 60

tct ggg acc aag aag gag aac tgc ccg tac agc atc ctg gag ata aca 240
 Ser Gly Thr Lys Lys Glu Asn Cys Pro Tyr Ser Ile Leu Glu Ile Thr
 65 70 75 80

tca gta gaa atc gga gtt gtt gcc gtc aaa gcc att aac agc aac tat 288
 Ser Val Glu Ile Gly Val Val Ala Val Lys Ala Ile Asn Ser Asn Tyr
 85 90 95

tac tta gcc atg aac aag aag ggg aaa ctc tat ggc tca aaa gaa ttt 336
 Tyr Leu Ala Met Asn Lys Lys Gly Lys Leu Tyr Gly Ser Lys Glu Phe
 100 105 110

aac aat gac tgt aag ctg aag 357
 Asn Asn Asp Cys Lys Leu Lys
 115

<210> 80
 <211> 119
 <212> PRT
 <213> Homo sapiens

<400> 80
 Met Thr Cys Gln Ala Leu Gly Gln Asp Met Val Ser Pro Glu Ala Thr
 1 5 10 15

Asn Ser Ser Ser Ser Ser Phe Ser Ser Pro Ser Ser Ala Gly Arg His
 20 25 30

Val Arg Ser Tyr Asn His Leu Gln Gly Asp Val Arg Trp Arg Lys Leu
 35 40 45

Phe Ser Phe Thr Lys Tyr Phe Leu Lys Ile Glu Lys Asn Gly Lys Val
 50 55 60

Ser Gly Thr Lys Lys Glu Asn Cys Pro Tyr Ser Ile Leu Glu Ile Thr
 65 70 75 80

Ser Val Glu Ile Gly Val Val Ala Val Lys Ala Ile Asn Ser Asn Tyr
 85 90 95

Tyr Leu Ala Met Asn Lys Lys Gly Lys Leu Tyr Gly Ser Lys Glu Phe
 100 105 110

Asn Asn Asp Cys Lys Leu Lys
 115

<210> 81
 <211> 276
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(276)

<400> 81
 atg gct ggt cgt cac gtt cgt tct tac aac cac ctg cag ggt gac gtt 48
 Met Ala Gly Arg His Val Arg Ser Tyr Asn His Leu Gln Gly Asp Val
 1 5 10 15

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cgt tgg cgt aaa ctg ttc tct ttc acc aaa tac ttc ctg aaa atc gaa 96
Arg Trp Arg Lys Leu Phe Ser Phe Thr Lys Tyr Phe Leu Lys Ile Glu
      20                      25                      30

aaa aac ggt aaa gtt tct ggg acc aag aag gag aac tgc ccg tac agc 144
Lys Asn Gly Lys Val Ser Gly Thr Lys Lys Glu Asn Cys Pro Tyr Ser
      35                      40                      45

atc ctg gag ata aca tca gta gaa atc gga gtt gtt gcc gtc aaa gcc 192
Ile Leu Glu Ile Thr Ser Val Glu Ile Gly Val Val Ala Val Lys Ala
      50                      55                      60

att aac agc aac tat tac tta gcc atg aac aag aag ggg aaa ctc tat 240
Ile Asn Ser Asn Tyr Tyr Leu Ala Met Asn Lys Lys Gly Lys Leu Tyr
      65                      70                      75                      80

ggc tca aaa gaa ttt aac aat gac tgt aag ctg aag 276
Gly Ser Lys Glu Phe Asn Asn Asp Cys Lys Leu Lys
      85                      90

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<210> 82
 <211> 92
 <212> PRT
 <213> Homo sapiens

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<400> 82
Met Ala Gly Arg His Val Arg Ser Tyr Asn His Leu Gln Gly Asp Val
  1                      5                      10                      15

Arg Trp Arg Lys Leu Phe Ser Phe Thr Lys Tyr Phe Leu Lys Ile Glu
      20                      25                      30

Lys Asn Gly Lys Val Ser Gly Thr Lys Lys Glu Asn Cys Pro Tyr Ser
      35                      40                      45

Ile Leu Glu Ile Thr Ser Val Glu Ile Gly Val Val Ala Val Lys Ala
      50                      55                      60

Ile Asn Ser Asn Tyr Tyr Leu Ala Met Asn Lys Lys Gly Lys Leu Tyr
      65                      70                      75                      80

Gly Ser Lys Glu Phe Asn Asn Asp Cys Lys Leu Lys
      85                      90

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<210> 83
 <211> 525
 <212> DNA
 <213> Homo sapiens

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<400> 83
atgacctctc aggcctctggg tcaggacatg gtttctccgg aagctaccaa ctcttctct 60
tcctctttct ctccccgctc ttccgctggt cgtcacgttc gttcttacia ccacctgcag 120
ggtgacgttc gttggcgtaa actggttctt ttcaccaaact acttcttgaa aatcgaaaaa 180
aacggtaaaag tttctgggac caagaaggag aactctccgt acagcatcct ggagataaca 240
tcagtagaaa tcggagttgt tgccgtcaaa gccattaaca gcaactatta cttagccatg 300
aacaagaagg ggaaactcta tggctcaaaa gaatttaaca atgactgtaa gctgaaggag 360
aggatagagg aaaatggata caatacctat gcatcattta actggcagca taatgggagg 420
caaatgtatg tggcattgaa tggaaaagga gctccaagga gaggacagaa aacacgaagg 480
aaaaacacct ctgctcactt tcttccaatg gtggtacact catag 525

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<210> 84
<211> 525
<212> DNA
<213> Homo sapiens

<400> 84
atgacctgcc aggcctctggg tcaggacatg gtttctccgg aagctaccaa ctcttcctct 60
tcctctttct cttccccgtc ttccgctggt cgtcacgttc gttcttacia ccacctgcag 120
ggtgacgttc gttggcgtaa actgttctct ttcaccaaact acttcctgaa aatcgaaaaa 180
aacggtaaaag tttctgggac caagaaggag aactctccgt acagcatcct ggagataaca 240
tcagtagaaa tcggagttgt tgccgtcaaa gccattaaca gcaactatta cttagccatg 300
aacaagaagg ggaaactcta tggctcaaaa gaatttaaca atgactgtaa gctgaaggag 360
aggatagagg aaaatggata caatacctat gcatcattta actggcagca taatgggagg 420
caaattgtatg tggcattgaa tggaaaagga gctccaagga gaggacagaa aacacgaagg 480
aaaaacacct ctgctcactt tcttccaatg gtggtacact catag 525

<210> 85
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 85
ggacctcat gacctctcag gctctgggt 29

<210> 86
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 86
aaggagaact ctccgtacag c 21

<210> 87
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 87
gctgtacggt ctgttctcct t 21

<210> 88
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 88
ggaccctcat gacctgccag gctctgggtc aggac 35

<210> 89
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 89
ctgccaagc ttattatgag tgtaccacca ttggaag 37

<210> 90
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 90
aaagatcct gccaggctct gggtcaggac atg 33

<210> 91
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 91
gcggcacatg tcttacaacc acctgcaggg tg 32

<210> 92
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 92
gggccaagc ttatgagtgt accaccat 28

<210> 93
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 93
ccggcggatc ccatatgtct tacaaccacc tgcagg 36

<210> 94
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 94
ccggcggtac cttattatga gtgtaccacc attgg 35

<210> 95
<211> 426
<212> DNA
<213> Homo sapiens

<400> 95
atgtcttaca accacctgca ggggtgacgtt cgttggcgta aactgttctc tttcaccaaa 60
tacttcctga aaatcgaaaa aaacggtaaa gtttctggga ccaagaagga gaactgcccg 120
tacagcatcc tggagataac atcagtagaa atcggagttg ttgccgtcaa agccattaac 180
agcaactatt acttagccat gaacaagaag gggaaactct atggctcaaa agaatttaac 240
aatgactgta agctgaagga gaggatagag gaaaatggat acaataccta tgcatacatt 300
aactggcagc ataatgggag gcaaattgtat gtggcattga atggaaaagg agctccaagg 360
agaggacaga aaacacgaag gaaaaacacc tctgctcact ttcttccaat ggtggtacac 420
tcataa 426

<210> 96
<211> 141
<212> PRT
<213> Homo sapiens

<400> 96
Met Ser Tyr Asn His Leu Gln Gly Asp Val Arg Trp Arg Lys Leu Phe
1 5 10 15
Ser Phe Thr Lys Tyr Phe Leu Lys Ile Glu Lys Asn Gly Lys Val Ser
20 25 30
Gly Thr Lys Lys Glu Asn Cys Pro Tyr Ser Ile Leu Glu Ile Thr Ser
35 40 45
Val Glu Ile Gly Val Val Ala Val Lys Ala Ile Asn Ser Asn Tyr Tyr
50 55 60
Leu Ala Met Asn Lys Lys Gly Lys Leu Tyr Gly Ser Lys Glu Phe Asn
65 70 75 80
Asn Asp Cys Lys Leu Lys Glu Arg Ile Glu Glu Asn Gly Tyr Asn Thr
85 90 95
Tyr Ala Ser Phe Asn Trp Gln His Asn Gly Arg Gln Met Tyr Val Ala
100 105 110
Leu Asn Gly Lys Gly Ala Pro Arg Arg Gly Gln Lys Thr Arg Arg Lys
115 120 125
Asn Thr Ser Ala His Phe Leu Pro Met Val Val His Ser
130 135 140

<210> 97
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<400> 97
caaccacctg cagggtgacg 20

<210> 98
<211> 78
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<400> 98
aacggtcgac aaatgtatgt ggcaactgaac ggtaaagggtg ctccacgtcg tggtcagaaa 60
acccgtcgtg aaaacacc 78

<210> 99
<211> 76
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<400> 99
gggcccaagc ttaagagtgt accaccattg gcagaaagtg agcagaggtg tttttacgac 60
gggttttctg accacg 76

<210> 100
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<400> 100
gccacataca tttgtcgacc gtt 23

<210> 101
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<400> 101
gggcccaagc ttaagagtg 19

<210> 102
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<400> 102
gccacataca tttgtcgacc gtt 23

<210> 103
<211> 90
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<400> 103
ctgcagggtg acgttcgttg gcgtaaaactg ttctccttca ccaaatactt cctgaaaatc 60
gaaaaaaacg gttaaagtctc tggtagcaag 90

<210> 104
<211> 90
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<400> 104
agctttaaca gcaacaacac cgatttcaac ggaggtgatt tccaggatgg agtacgggca 60
gttttctttc ttggtaccag aaactttacc 90

<210> 105
<211> 90
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<400> 105
ggtgttggtg ctgttaaagc tatcaactcc aactactacc tggctatgaa caagaaagg 60
aaactgtacg gttccaaaga atttaacaac 90

<210> 106
<211> 100
<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
oligonucleotide

<400> 106

gtcgaccgtt gtgctgccag ttgaaggaag cgtaggtgtt gtaaccgttt tcttcgatac 60
gttctttcag ttacagtcg ttgttaaatt ctttggaacc 100

<210> 107

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
oligonucleotide

<400> 107

gcggcgctcga ccgttgtgtc gccag 25

<210> 108

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
oligonucleotide

<400> 108

gcggcctgca ggtgacgtt cggttg 26

<210> 109

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
oligonucleotide

<400> 109

ccggcggatc ccatatgtct tacaaccacc tgcagg 36

<210> 110

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
oligonucleotide

<400> 110

cgcgcatat cttattaaga gtgtaccacc attg 34

<210> 111
<211> 426
<212> DNA
<213> Homo sapiens

<400> 111
atgtctttaca accacctgca ggggtgacgtt cgttggcgta aactgtttctc cttcaccaaa 60
tactttcctga aaatcgaaaa aaacggtaaa gtttctggta ccaagaaaga aaactgcccg 120
tactccatcc tggaaatcac ctccgttgaa atcgggtgtt ttgctgttaa agctatcaac 180
tccaactact acctggctat gaacaagaaa ggtaaactgt acggttccaa agaatttaac 240
aacgactgta aactgaaaga acgtatcgaa gaaaacgggtt acaacaccta cgcttccttc 300
aactggcagc acaacggtcg acaaattgtat gtggcactga acggtaaagg tgctccacgt 360
cgtgggcaga aaaccgcgcg taaaaacacc tctgctcact ttctgccaat ggtggtacac 420
tcttaa 426

<210> 112
<211> 141
<212> PRT
<213> Homo sapiens

<400> 112
Met Ser Tyr Asn His Leu Gln Gly Asp Val Arg Trp Arg Lys Leu Phe
1 5 10 15
Ser Phe Thr Lys Tyr Phe Leu Lys Ile Glu Lys Asn Gly Lys Val Ser
20 25 30
Gly Thr Lys Lys Glu Asn Cys Pro Tyr Ser Ile Leu Glu Ile Thr Ser
35 40 45
Val Glu Ile Gly Val Val Ala Val Lys Ala Ile Asn Ser Asn Tyr Tyr
50 55 60
Leu Ala Met Asn Lys Lys Gly Lys Leu Tyr Gly Ser Lys Glu Phe Asn
65 70 75 80
Asn Asp Cys Lys Leu Lys Glu Arg Ile Glu Glu Asn Gly Tyr Asn Thr
85 90 95
Tyr Ala Ser Phe Asn Trp Gln His Asn Gly Arg Gln Met Tyr Val Ala
100 105 110
Leu Asn Gly Lys Gly Ala Pro Arg Arg Gly Gln Lys Thr Arg Arg Lys
115 120 125
Asn Thr Ser Ala His Phe Leu Pro Met Val Val His Ser
130 135 140

<210> 113
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<400> 113
cgcgccatg gctctgggtc aggacatg

<210> 114
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<400> 114
gggcccaagc ttatgagtgt accaccat

28

<210> 115
<211> 516
<212> DNA
<213> Homo sapiens

<400> 115
atggctctgg gtcaagatat gggtttctccg gaagctacca actcttctctc ttcctcttttc 60
tcttccccgt cttccgctgg tcgtcacgtt cgttcttaca accacctgca ggggtgacgtt 120
cgttggcgta aactgttctc tttcaccaaa tacttctctga aaatcgaaaa aaacggtaaa 180
gtttctggga ccaagaagga gaactgcccg tacagcatcc tggagataac atcagtagaa 240
atcggagttg ttgccgtcaa agccattaac agcaactatt acttagccat gaacaagaa 300
gggaaactct atggctcaaa agaatttaac aatgactgta agctgaagga gaggatagag 360
gaaaatggat acaataccta tgcatcattt aactggcagc ataatgggag gcaaattgtat 420
gtggcattga atggaaaagg agctccaagg agaggacaga aaacacgaag gaaaaacacc 480
tctgctcact ttcttccaat ggtggtacac tcataa 516

<210> 116
<211> 171
<212> PRT
<213> Homo sapiens

<400> 116
Met Ala Leu Gly Gln Asp Met Val Ser Pro Glu Ala Thr Asn Ser Ser
1 5 10 15
Ser Ser Ser Phe Ser Ser Pro Ser Ser Ala Gly Arg His Val Arg Ser
20 25 30
Tyr Asn His Leu Gln Gly Asp Val Arg Trp Arg Lys Leu Phe Ser Phe
35 40 45
Thr Lys Tyr Phe Leu Lys Ile Glu Lys Asn Gly Lys Val Ser Gly Thr
50 55 60
Lys Lys Glu Asn Cys Pro Tyr Ser Ile Leu Glu Ile Thr Ser Val Glu
65 70 75 80
Ile Gly Val Val Ala Val Lys Ala Ile Asn Ser Asn Tyr Tyr Leu Ala
85 90 95
Met Asn Lys Lys Gly Lys Leu Tyr Gly Ser Lys Glu Phe Asn Asn Asp
100 105 110
Cys Lys Leu Lys Glu Arg Ile Glu Glu Asn Gly Tyr Asn Thr Tyr Ala
115 120 125
Ser Phe Asn Trp Gln His Asn Gly Arg Gln Met Tyr Val Ala Leu Asn
130 135 140

Gly Lys Gly Ala Pro Arg Arg Gly Gln Lys Thr Arg Arg Lys Asn Thr
145 150 155 160

Ser Ala His Phe Leu Pro Met Val Val His Ser
165 170

<210> 117
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 117
gcggcacatg tcttacaacc acctgcaggg tg 32

<210> 118
<211> 75
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 118
ctgcccgaagc ttttatgagt gtaccacccat tggaagaaag tgagcagagg tgtttttttc 60
tcgtgttttc tgtcc 75

<210> 119
<211> 426
<212> DNA
<213> Homo sapiens

<400> 119
atgtctttaca accacctgca ggggtgacgtt cgttggcgta aactgtttctc tttcaccaaa 60
tacttccctga aaatcgaaaa aaacggtaaa gtttctggga ccaagaagga gaactgccccg 120
tacagcatcc tggagataac atcagtagaa atcggagttg ttgccgtcaa agccattaac 180
agcaactatt acttagccat gaacaagaag gggaaactct atggctcaaa agaatttaac 240
aatgactgta agctgaagga gaggatagag gaaaatggat acaataccta tgcattcattt 300
aactggcagc ataatgggag gcaaatgtat gtggcattga atggaaaagg agctccaagg 360
agaggacaga aaacacgaga aaaaaacacc tctgctcact ttcttccaat ggtggtacac 420
tcatag 426

<210> 120
<211> 141
<212> PRT
<213> Homo sapiens

<400> 120
Met Ser Tyr Asn His Leu Gln Gly Asp Val Arg Trp Arg Lys Leu Phe
1 5 10 15

Ser Phe Thr Lys Tyr Phe Leu Lys Ile Glu Lys Asn Gly Lys Val Ser
20 25 30

Gly Thr Lys Lys Glu Asn Cys Pro Tyr Ser Ile Leu Glu Ile Thr Ser
35 40 45

Val	Glu	Ile	Gly	Val	Val	Ala	Val	Lys	Ala	Ile	Asn	Ser	Asn	Tyr	Tyr
50						55					60				
Leu	Ala	Met	Asn	Lys	Lys	Gly	Lys	Leu	Tyr	Gly	Ser	Lys	Glu	Phe	Asn
65					70					75					80
Asn	Asp	Cys	Lys	Leu	Lys	Glu	Arg	Ile	Glu	Glu	Asn	Gly	Tyr	Asn	Thr
			85						90					95	
Tyr	Ala	Ser	Phe	Asn	Trp	Gln	His	Asn	Gly	Arg	Gln	Met	Tyr	Val	Ala
			100					105					110		
Leu	Asn	Gly	Lys	Gly	Ala	Pro	Arg	Arg	Gly	Gln	Lys	Thr	Arg	Glu	Lys
		115					120					125			
Asn	Thr	Ser	Ala	His	Phe	Leu	Pro	Met	Val	Val	His	Ser			
130						135						140			

<210> 121
 <211> 32
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

<400> 121
 gcggcacatg tcttacaacc acctgcaggg tg 32

<210> 122
 <211> 75
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

<400> 122
 ctgcccaagc ttttatgagt gtaccacat tggaagaaag tgagcagagg tgtttttctg 60
 tcgtgttttc tgtcc 75

<210> 123
 <211> 426
 <212> DNA
 <213> Homo sapiens

<400> 123
 atgtcttaca accacctgca gggtagcgtt cgttggcgta aactgttctc tttcaccaaa 60
 tacttcctga aaatcgaaaa aaacggtaaa gtttctggga ccaagaagga gaactgcccg 120
 tacagcatcc tggagataac atcagtagaa atcggagttg ttgccgtcaa agccattaac 180
 agcaactatt acttagccat gaacaagaag gggaaactct atggctcaaa agaatttaac 240
 aatgactgta agctgaagga gaggatagag gaaaatggat acaataccta tgcattcattt 300
 aactggcagc ataatgggag gcaaatgtat gtggcattga atggaaaagg agctccaagg 360
 agaggacaga aaacacgaca gaaaaacacc tctgctcact ttcttccaat ggtggtacac 420
 tcatag 426

<210> 124
 <211> 141

<212> PRT

<213> Homo sapiens

<400> 124

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Met Ser Tyr Asn His Leu Gln Gly Asp Val Arg Trp Arg Lys Leu Phe
 1           5           10           15

Ser Phe Thr Lys Tyr Phe Leu Lys Ile Glu Lys Asn Gly Lys Val Ser
          20           25           30

Gly Thr Lys Lys Glu Asn Cys Pro Tyr Ser Ile Leu Glu Ile Thr Ser
          35           40           45

Val Glu Ile Gly Val Val Ala Val Lys Ala Ile Asn Ser Asn Tyr Tyr
 50           55           60

Leu Ala Met Asn Lys Lys Gly Lys Leu Tyr Gly Ser Lys Glu Phe Asn
65           70           75           80

Asn Asp Cys Lys Leu Lys Glu Arg Ile Glu Glu Asn Gly Tyr Asn Thr
          85           90           95

Tyr Ala Ser Phe Asn Trp Gln His Asn Gly Arg Gln Met Tyr Val Ala
          100          105          110

Leu Asn Gly Lys Gly Ala Pro Arg Arg Gly Gln Lys Thr Arg Gln Lys
          115          120          125

Asn Thr Ser Ala His Phe Leu Pro Met Val Val His Ser
          130          135          140

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<210> 125

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 125

gcggcacatg tcttacaacc acctgcaggg tg

32

<210> 126

<211> 84

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 126

ctgcccaagc ttttatgagt gtaccacat tggaagaaag tgagcagagg tgtttttcc 60
tcgtgtttcc tgcctctcc ttgg 84

<210> 127

<211> 426

<212> DNA

<213> Homo sapiens

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<400> 127
atgtcttaca accacctgca ggggtgacgtt cgttggcgta aactgttctc tttcaccaaa 60
tacttcctga aaatcgaaaa aaacggtaaa gtttctggga ccaagaagga gaactgcccg 120
tacagcatcc tggagataac atcagtagaa atcggagttg ttgccgtcaa agccattaac 180
agcaactatt acttagccat gaacaagaag gggaaactct atggctcaaa agaatttaac 240
aatgactgta agctgaagga gaggatagag gaaaatggat acaataccta tgcattcatt 300
aactggcagc ataatgggag gcaaattgtat gtggcattga atggaaaagg agctccaagg 360
agaggacagg aaacacgaag gaaaaacacc tctgctcact ttcttccaat ggtggtacac 420
tcatag 426
```

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<210> 128
<211> 141
<212> PRT
<213> Homo sapiens
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<400> 128
Met Ser Tyr Asn His Leu Gln Gly Asp Val Arg Trp Arg Lys Leu Phe
  1              5              10              15

Ser Phe Thr Lys Tyr Phe Leu Lys Ile Glu Lys Asn Gly Lys Val Ser
      20              25              30

Gly Thr Lys Lys Glu Asn Cys Pro Tyr Ser Ile Leu Glu Ile Thr Ser
      35              40              45

Val Glu Ile Gly Val Val Ala Val Lys Ala Ile Asn Ser Asn Tyr Tyr
      50              55              60

Leu Ala Met Asn Lys Lys Gly Lys Leu Tyr Gly Ser Lys Glu Phe Asn
      65              70              75              80

Asn Asp Cys Lys Leu Lys Glu Arg Ile Glu Glu Asn Gly Tyr Asn Thr
      85              90              95

Tyr Ala Ser Phe Asn Trp Gln His Asn Gly Arg Gln Met Tyr Val Ala
      100              105              110

Leu Asn Gly Lys Gly Ala Pro Arg Arg Gly Gln Glu Thr Arg Arg Lys
      115              120              125

Asn Thr Ser Ala His Phe Leu Pro Met Val Val His Ser
      130              135              140
```

```
<210> 129
<211> 32
<212> DNA
<213> Artificial Sequence
```

```
<220>
<223> Description of Artificial Sequence: primer
```

```
<400> 129
gcggcacatg tcttacaacc acctgcaggg tg 32
```

```
<210> 130
<211> 84
<212> DNA
<213> Artificial Sequence
```

<220>

<223> Description of Artificial Sequence: primer

<400> 130

ctgcccgaagc ttttatgagt gtaccacccat tggaagaaag tgagcagagg tgtttttcct 60
tcgtgtctgc tgcctctcc ttgg 84

<210> 131

<211> 426

<212> DNA

<213> Homo sapiens

<400> 131

atgtccttaca accacctgca ggggtgacgtt cgttggcgta aactgttctc tttcaccaaa 60
tacttctctga aaatcgaaaa aaacggtaaa gtttctggga ccaagaagga gaactgcccg 120
tacagcatcc tggagataac atcagtagaa atcggagttg ttgccgtcaa agccattaac 180
agcaactatt acttagccat gaacaagaag gggaaactct atggctcaaa agaatttaac 240
aatgactgta agctgaagga gaggatagag gaaaatggat acaataccta tgcattcattt 300
aactggcagc ataatgggag gcaaattgtat gtggcattga atggaaaagg agctccaagg 360
agaggacagc agacacgaag gaaaaacacc tctgctcact ttcttccaat ggtggtacac 420
tcatag 426

<210> 132

<211> 141

<212> PRT

<213> Homo sapiens

<400> 132

Met Ser Tyr Asn His Leu Gln Gly Asp Val Arg Trp Arg Lys Leu Phe
1 5 10 15
Ser Phe Thr Lys Tyr Phe Leu Lys Ile Glu Lys Asn Gly Lys Val Ser
20 25 30
Gly Thr Lys Lys Glu Asn Cys Pro Tyr Ser Ile Leu Glu Ile Thr Ser
35 40 45
Val Glu Ile Gly Val Val Ala Val Lys Ala Ile Asn Ser Asn Tyr Tyr
50 55 60
Leu Ala Met Asn Lys Lys Gly Lys Leu Tyr Gly Ser Lys Glu Phe Asn
65 70 75 80
Asn Asp Cys Lys Leu Lys Glu Arg Ile Glu Glu Asn Gly Tyr Asn Thr
85 90 95
Tyr Ala Ser Phe Asn Trp Gln His Asn Gly Arg Gln Met Tyr Val Ala
100 105 110
Leu Asn Gly Lys Gly Ala Pro Arg Arg Gly Gln Gln Thr Arg Arg Lys
115 120 125
Asn Thr Ser Ala His Phe Leu Pro Met Val Val His Ser
130 135 140

<210> 133

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 133

gcggcacatg tcttacaacc acctgcaggg tg

32

<210> 134

<211> 93

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 134

ctgcccgaagc ttttatgagt gtaccacccat tggaagaaag tgagcagagg tgtttttcct 60
tcgtgttttc tgccttccc ttggagctcc ttt 93

<210> 135

<211> 426

<212> DNA

<213> Homo sapiens

<400> 135

atgtcttaca accacctgca ggggtgacgtt cggtggcgta aactgttctc tttcaccaaa 60
tacttcctga aaatcgaaaa aaacggtaaa gtttctggga ccaagaagga gaactgcccg 120
tacagcatcc tggagataac atcagtagaa atcggagttg ttgccgtcaa agccattaac 180
agcaactatt acttagccat gaacaagaag gggaaactct atggctcaaa agaatttaac 240
aatgactgta agctgaagga gaggatagag gaaaatggat acaataccta tgcattcatt 300
aactggcagc ataatgggag gcaaattgtat gtggcattga atggaaaagg agctccaagg 360
gaaggacaga aaacacgaag gaaaaacacc tctgctcact ttcttccaat ggtggtacac 420
tcatag 426

<210> 136

<211> 140

<212> PRT

<213> Homo sapiens

<400> 136

Met Tyr Asn His Leu Gln Gly Asp Val Arg Trp Arg Lys Leu Phe Ser
1 5 10 15
Phe Thr Lys Tyr Phe Leu Lys Ile Glu Lys Asn Gly Lys Val Ser Gly
20 25 30
Thr Lys Lys Glu Asn Cys Pro Tyr Ser Ile Leu Glu Ile Thr Ser Val
35 40 45
Glu Ile Gly Val Val Ala Val Lys Ala Ile Asn Ser Asn Tyr Tyr Leu
50 55 60
Ala Met Asn Lys Lys Gly Lys Leu Tyr Gly Ser Lys Glu Phe Asn Asn
65 70 75 80
Asp Cys Lys Leu Lys Glu Arg Ile Glu Glu Asn Gly Tyr Asn Thr Tyr
85 90 95
Ala Ser Phe Asn Trp Gln His Asn Gly Arg Gln Met Tyr Val Ala Leu
100 105 110

Asn Gly Lys Gly Ala Pro Arg Glu Gly Gln Lys Thr Arg Arg Lys Asn
115 120 125

Thr Ser Ala His Phe Leu Pro Met Val Val His Ser
130 135 140

<210> 137
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 137
gcggcacatg tcttacaacc acctgcaggg tg 32

<210> 138
<211> 93
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 138
ctgcccgaagc ttttatgagt gtaccacccat tggaagaaag tgagcagagg tgtttttcct 60
tcgtgttttc tgcctctgcc ttggagctcc ttt 93

<210> 139
<211> 426
<212> DNA
<213> Homo sapiens

<400> 139
atgtctttaca accacctgca ggggtgacgtt cggtggcgta aactgttctc tttcaccaaa 60
tacttcctga aaatcgaaaa aaacggtaaa gtttctggga ccaagaagga gaactgcccg 120
tacagcatcc tggagataac atcagtagaa atcggagttg ttgccgtcaa agccattaac 180
agcaactatt acttagccat gaacaagaag gggaaactct atggctcaaa agaatttaac 240
aatgactgta agctgaagga gaggatagag gaaaatggat acaataccta tgcattcatt 300
aactggcagc ataatgggag gcaaattgtat gtggcattga atggaaaagg agtccaagg 360
cagggacaga aaacacgaag gaaaaacacc tctgctcact ttcttccaat ggtggtacac 420
tcatag 426

<210> 140
<211> 141
<212> PRT
<213> Homo sapiens

<400> 140
Met Ser Tyr Asn His Leu Gln Gly Asp Val Arg Trp Arg Lys Leu Phe
1 5 10 15

Ser Phe Thr Lys Tyr Phe Leu Lys Ile Glu Lys Asn Gly Lys Val Ser
20 25 30

Gly Thr Lys Lys Glu Asn Cys Pro Tyr Ser Ile Leu Glu Ile Thr Ser
35 40 45

Val Glu Ile Gly Val Val Ala Val Lys Ala Ile Asn Ser Asn Tyr Tyr
50 55 60
Leu Ala Met Asn Lys Lys Gly Lys Leu Tyr Gly Ser Lys Glu Phe Asn
65 70 75 80
Asn Asp Cys Lys Leu Lys Glu Arg Ile Glu Glu Asn Gly Tyr Asn Thr
85 90 95
Tyr Ala Ser Phe Asn Trp Gln His Asn Gly Arg Gln Met Tyr Val Ala
100 105 110
Leu Asn Gly Lys Gly Ala Pro Arg Gln Gly Gln Lys Thr Arg Arg Lys
115 120 125
Asn Thr Ser Ala His Phe Leu Pro Met Val Val His Ser
130 135 140

<210> 141
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 141
gcggcacatg tcttacaacc acctgcaggg tg 32

<210> 142
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 142
ttgaatggag aaggagctcc a 21

<210> 143
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 143
tggagctcct tctccattca a 21

<210> 144
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 144
ctgcccaagc ttttatgagt gtaccaccat tgg 33

<210> 145
<211> 426
<212> DNA
<213> Homo sapiens

<400> 145
atgtcttaca accacctgca ggggtgacgtt cggtggcgta aactgttctc tttcaccaaa 60
tacttcctga aaatcgaaaa aaacggtaaa gtttctggga ccaagaagga gaactgcccg 120
tacagcatcc tggagataac atcagtagaa atcggagttg ttgccgtcaa agccattaac 180
agcaactatt acttagccat gaacaagaag gggaaactct atggctcaaa agaatttaac 240
aatgactgta agctgaagga gaggatagag gaaaatggat acaataccta tgcatacatt 300
aactggcagc ataatgggag gcaaattgtat gtggcattga atggagaagg agtccaagg 360
agaggacaga aaacacgaag gaaaaacacc tctgctcact ttcttccaat ggtggtacac 420
tcatag 426

<210> 146
<211> 141
<212> PRT
<213> Homo sapiens

<400> 146
Met Ser Tyr Asn His Leu Gln Gly Asp Val Arg Trp Arg Lys Leu Phe
1 5 10 15
Ser Phe Thr Lys Tyr Phe Leu Lys Ile Glu Lys Asn Gly Lys Val Ser
20 25 30
Gly Thr Lys Lys Glu Asn Cys Pro Tyr Ser Ile Leu Glu Ile Thr Ser
35 40 45
Val Glu Ile Gly Val Val Ala Val Lys Ala Ile Asn Ser Asn Tyr Tyr
50 55 60
Leu Ala Met Asn Lys Lys Gly Lys Leu Tyr Gly Ser Lys Glu Phe Asn
65 70 75 80
Asn Asp Cys Lys Leu Lys Glu Arg Ile Glu Glu Asn Gly Tyr Asn Thr
85 90 95
Tyr Ala Ser Phe Asn Trp Gln His Asn Gly Arg Gln Met Tyr Val Ala
100 105 110
Leu Asn Gly Glu Gly Ala Pro Arg Arg Gly Gln Lys Thr Arg Arg Lys
115 120 125
Asn Thr Ser Ala His Phe Leu Pro Met Val Val His Ser
130 135 140

<210> 147
<211> 3974
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: pHE4-5 vector

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<400> 147
ggtacctaag tgagtagggc gtccgatcga cggacgcctt ttttttgaat tcgtaatcat 60
ggtcatagct gtttcctgtg tgaaattggt atccgctcac aattccacac aacatacgag 120
ccggaagcat aaagtgtaaa gcctgggggt cctaagttagt gagctaactc acattaattg 180
cgttgcgctc actgcccgtt ttccagtcgg gaaacctgtc gtgccagctg cattaatgaa 240
tcggccaacg cgcggggaga ggcggtttgc gtattgggag ctcttcgctc tcctcgctca 300
ctgactcgct gcgctcggtc gttcggtgcg ggcgagcggt atcagctcac tcaaaggcgg 360
taatacgggt atccacagaa tcaggggata acgcaggaaa gaacatgtga gcaaaaggcc 420
agcaaaaggc caggaaccgt aaaaaggccg cgttgctggc gtttttccat aggctccgcc 480
ccccgacga gcatcacaaa aatcgacgct caagtccagag gtggcgaaac ccgacaggac 540
tataaagata ccaggcgttt cccctggaa gctccctcgt gcgctctcct gttccgaccc 600
tgccgcttac cggatacctg tccgccttcc tcccttcggg aagcgtggcg ctttctcata 660
gctcacgctg taggtatctc agttcggtgt aggtcgttcg ctccaagctg ggctgtgtgc 720
acgaaccccc cgttcagccc gaccgctgcg ccttatccgg taactatcgt cttgagtcca 780
acccggtaag acacgactta tcgccactgg cagcagccac tggtaacagg attagcagag 840
cgaggtatgt aggcggtgct acagagttct tgaagtgggt gcctaactac ggctacacta 900
gaagaacagt attttgatc tgcgctctgc tgaagccagt taccttcgga aaaagagttg 960
gtagctcttg atccggcaaa caaaccaccg ctggtagcgg tgggtttttt gtttgcaagc 1020
agcagattac gcgcagaaaa aaaggatctc aagaagatcc tttgatcttt tctacggggt 1080
ctgacgctca gtggaacgaa aactcacgtt aagggatttt ggtcatgaga ttatcgctca 1140
caattcgcgc gcgaaggcga agcggcatgc atttacgttg acaccatcga atggtgcaaa 1200
acctttcgcg gtatggcatg atagcgcccg gaagagagtc aattcagggt ggtgaatgtg 1260
aaaccagtaa cgttatacga tgtcgagag tatgcccgtg tctcttatca gaccgtttcc 1320
cgcgtgggtg accaggccag ccacgtttct gcgaaaacgc gggaaaaagt ggaagcggcg 1380
atggcgagc tgaattacat tcccaaccgc gtggcacaa aactggcggg caaacagtcg 1440
ttgctgattg gcgttgccac ctccagctcg gccctgcacg cgccgtcgca aattgtcgcg 1500
gcgattaaat ctgcgcgcga tcaactgggt gccagcgtgg tgggtgctgat ggtagaacga 1560
agcggcgctc aagcctgtaa agcggcgggt cacaatcttc tcgcgcaacg cgtcagtggg 1620
ctgatcatta actatccgct ggatgaccag gatgccattg ctgtggaagc tgctgcact 1680
aatgttccgg cgttatttct tgatgtctct gaccagacac ccatcaacag tattattttc 1740
tcccataag acggtacgcg actggcggtg gagcatctgg tcgcattggg tcaccagcaa 1800
atcgcgctgt tagcgggccc attaatgtct gtctcggcgc gtctgcgtct ggctggctgg 1860
cataaatatc tcaactcgaa tcaaattcag ccgatagcgg aacgggaagg cgactggagt 1920
gccatgtccg gttttcaaca aaccatgcaa atgtggaatg agggcatcgt tcccactgcg 1980
atgctgggtg ccaacgatca gatggcgctg ggcgcaatgc gcgccattac cgagtcgggg 2040
ctgcgcgttg gtgcggatat ctcggtagt gaccagacag gattttcgcc tgctggggca aaccagcgtg 2100
tatatccgc cgtaaacacg catcaaacag gcttttcgcc tgcgtgggca aaccagcgtg 2160
gaccgcttgc tgcaactctc tcagggccag gcggtgaagg gcaatcagct gttgcccgtc 2220
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ttggccgatt cattaatgca gctggcacga caggtttccc gactggaaaag cgggcagtga 2340
gcgcaacgca attaatgtaa gttagcgca attgtcgacc aaagcggcca tcgtgectcc 2400
ccactcctgc agttcggggg catggatgcg cggatagcgg ctgctggttt ctggtatgcc 2460
gacggaattg cactgcccgt agaactccgc gaggtcgctc agcctcaggc agcagctgaa 2520
ccaactcgcg aggggatcga gcccggggtg ggcgaagaac tccagcatga gatccccgcg 2580
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ggcggcggtg gaatcgaaat ctcgatgatg caggttgggc gtcgcttggt cggtcatttc 2700
gaaccccgag gtcccgtcga gaagaactcg tcaagaaggc gatagaaggc gatgcgctgc 2760
gaatcgggag cggcgatacc gtaaaagcac aggaagcggg cagcccatc gccgccaagc 2820
tcttcagcaa tatcacgggt agccaacgct atgtcctgat agcgggtccg cacacccagc 2880
cggccacagt cgtgaatcc agaaaagcgg ccattttcca ccatgatatt cggcaagcag 2940
gcatcgccat gggtcacgac gagatcctcg ccgtcgggca tgcgcgcctt gagcctggcg 3000
aacagttcgg ctggcgcgag cccctgatgc tcttcgtcca gatcatcctg atcgacaaga 3060
ccggttcca tccgagtacg tgctcgctcg atgcgatgtt tcgcttggtg gtcgaatggg 3120
caggtagccg gatcaagcgt atgcagccgc cgcattgcat cagccatgat ggatactttc 3180
tcggcaggag caaggtgaga tgacaggaga tccctgcccc gcacttcgcc caatagcagc 3240
cagtccttc ccgcttcagt gacaacgtcg agcacagctg cgcaaggaa gcccgtcgtg 3300
gccagccacg atagccgcgc tgccctcgcc tcgagttcat tcagggcacc ggacaggtcg 3360
gtcttgacaa aaagaaccgg gcgcccctgc gctgacagcc ggaacacggc ggcacagag 3420
cagccgattg tctgttgtgc ccagtcatag ccgaatagcc tctccacca agcggccgga 3480
gaacctgcgt gcaatccatc ttgttcaatc atgcgaaacg atcctcatcc tgtctcttga 3540
tcagatcttg atccccctgc ccatacagatc cttggcgga agaaagccat ccagtttact 3600
ttgcagggct tcccacacct accagagggc gccccagctg gcaattccgg ttcgcttgct 3660

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gtccataaaa cgcgccagtc tagctatcgc catgtaagcc cactgcaagc tacctgcttt 3720
ctctttgcgc ttgcgttttc ccttggtccag atagcccagt agctgacatt catccggggg 3780
cagcaccggt tctgcggact ggctttctac gtgttcgct tccttttagca gcccttgccg 3840
cctgagtgc tgcggcagcg tgaagcttaa aaaactgcaa aaaatagttt gacttggtgag 3900
cggataacaa ttaagatgta cccaattgtg agcggataac aatttcacac attaaagagg 3960
agaaattaca tatg 3974
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<210> 148
 <211> 112
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: pHE4-5
 promoter sequence

```
<400> 148
aagcttaaaa aactgcaaaa aatagtttga cttgtgagcg gataacaatt aagatgtacc 60
caattgtgag cggataacaa tttcacacat taaagaggag aaattacata tg 112
```

<210> 149
 <211> 106
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

```
<400> 149
gagcgcggat cgcgccacat gaaggtctcc gtggctgccc tctcctgcct catgcttggt 60
actgcccttg gatctcaggc cagctacaat caccttcaag gagatg 106
```

<210> 150
 <211> 36
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

```
<400> 150
gagcgcggat ccctatgagt gtaccacat tggaag 36
```

<210> 151
 <211> 32
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

```
<400> 151
ccggccatat gcgtaaactg ttctctttca cc 32
```

<210> 152
 <211> 35
 <212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 152

ccggcggtac cttattatga gtgtaccacc attgg

35

<210> 153

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 153

gatcgccata tggctggtcg tcacgttcgt tc

32

<210> 154

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 154

gatcgcggtgta cttattatg agtgtaccac cattggaag

39

<210> 155

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 155

gatcgccata tggctggtcg tcacgttcgt tc

32

<210> 156

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 156

gatcgcggtgta cttattatg agtgtaccac cattggaag

39

<210> 157

<211> 32

<212> DNA

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 157
gatcgccata tggctggtcg tcacgttcgt tc 32

<210> 158
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 158
gatcgcggtgta ccttattatg agtgtaccac cattggaag 39

<210> 159
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 159
gatcgccata tggctggtcg tcacgttcgt tc 32

<210> 160
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 160
gatcgcggtgta ccttattatg agtgtaccac cattggaag 39

<210> 161
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 161
gatcgcggtat ccgccaccat gtggaaatgg atactgacac attgtgc 47

<210> 162
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 162
gatcgctcta gattatgagt gtaccaccat tggaagaaag 40

<210> 163
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 163
gatcgcggtat ccgccaccat gtggaaatgg atactgacac attgtgc 47

<210> 164
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 164
gatcgctcta gattatgagt gtaccaccat tggaagaaag 40

<210> 165
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 165
gatcgcggtat ccgccaccat gtggaaatgg atactgacac attgtgc 47

<210> 166
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 166
gatcgctcta gattatgagt gtaccaccat tggaagaaag 40

<210> 167
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 167
gatcgcggtat ccgccaccat gtggaaatgg atactgacac attgtgc 47

<210> 168
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 168
gatcgctcta gattatgagt gtaccacat tggaagaaag 40

<210> 169
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 169
gatcgccata tggctggtcg tcacgttcgt tc 32

<210> 170
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 170
gatcgcgga ccttattatg agtgtaccac cattggaag 39

<210> 171
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 171
gatcgccata tggctggtcg tcacgttcgt tc 32

<210> 172
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 172
gatcgcgga ccttattatg agtgtaccac cattggaag 39

<210> 173

<211> 456
<212> DNA
<213> Escherichia coli

<400> 173
catatggctg gtcgtcacgt tcgtttcttac aaccacctgc aggggtgacgt tcgttggcgt 60
aaactgttct ctttcaccaa atacttctctg aaaatcgaaa aaaacggtaa agtttctggg 120
accaagaagg agaactgccc gtacagcatc ctggagataa catcagtaga aatcggagtt 180
gttgccgtca aagccattaa cagcaactat tacttagcca tgaacaagaa ggggaaactc 240
tatggctcaa aagaatttaa caatgactgt aagctgaagg agaggataga ggaaaatgga 300
tacaatacct atgcatcatt taactggcag cataatggga ggcaaatgta tgtggcattg 360
aatggaaaag gagctccaag gagaggacag aaaacacgaa ggaaaaacac ctctgctcac 420
tttcttccaa tgggtgtaca ctcataataa ggtacc 456

<210> 174
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 174
gactacatat ggctggctgt cacgttcgtt cttacaacca cctgcagg 48

<210> 175
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 175
ctagtctcta gattattatg agtgtacaac catcggcagg aagtgag 47

<210> 176
<211> 447
<212> DNA
<213> Escherichia coli

<400> 176
atggctggtc gtcacgttcg ttcttacaac cacctgcagg gtgacgttcg ttggcgtaaa 60
ctgttctctt tcaccaaata cttcctgaaa atcgaaaaga acggtaaaag ttctggtacc 120
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